

SEQUENCE LISTING

<110> Pompejus, Markus
 Kroger, Burkhard
 Schroder, Hartwig
 Zelder, Oskar
 Haberhauer, Gregor
 Kim, Jun-Won
 Lee, Heung-Schick
 Hwang, Byung-Joon

<120> CORYNEBACTERIUM GLUTAMICUM GENES ENCODING
 METABOLIC PATHWAY PROTEINS

<130> BGI-121CP2

<140>

<141>

<150> (9)605740
 (1.1) 2000-06-23

<150> (9)603124
 (1.1) 2000-06-23

<150> (6)141031
 (1.1) 1999-06-25

<150> (6)142101
 (1.1) 1999-07-02

<150> (6)148613
 (1.1) 1999-08-12

<150> (6)187970
 (1.1) 2000-03-09

<150> DE 19931420.9
 (1.1) 1999-07-08

<160> 125

<170> PatentIn Vers. 2.0

<210> 1

<211> 1640

<212> DNA

<213> Corynebacterium glutamicum

<210>

<211> CDS

<212> (363)..(1676)

<400> 1

cacaaaactgt gtgcagaaat gcatgcagaa aaaggaaaagt tggggccaag atgggtgttt 60
 ctgtatgccc atgatcggat ctttgacagc tgggtatgcg acaaatcacc gagagtttgt 120
 aattcttaac aatggaaaag taacattgag agatgattta taccatcttg caccatttag 180
 agtgggggta gtatataccc cataacccta gctgtaacga atcgatttca aatcagttgg 240

aaaaagtc aa gaaaattacc cgagaattaa tttataccac acagttctatt gcaatagacc 300
 aagctgttca gtagggtgca tgggagaaga atttctaat aaaaactctt aaggacctcc 360
 aa atg cca aag tac gac aat tcc aat gct gac cag tgg ggc ttt gaa 407
 Met Pro Lys Tyr Asp Asn Ser Asn Ala Asp Gln Trp Gly Phe Glu
 1 5 10 15
 acc cgc tcc att cac gca ggc cag tca gta gac gca cag acc agc gca 455
 Thr Arg Ser Ile His Ala Gly Gln Ser Val Asp Ala Gln Thr Ser Ala
 20 25 30
 cga aac ctt ccg atc tac caa tcc acc gct ttc gtg ttc gac tcc gct 503
 Arg Asn Leu Pro Ile Tyr Gln Ser Thr Ala Phe Val Phe Asp Ser Ala
 35 40 45
 gag cac gcc aag cag cgt ttc gca ctt gag gat cta ggc cct gtt tac 551
 Glu His Ala Lys Gln Arg Phe Ala Leu Glu Asp Leu Gly Pro Val Tyr
 50 55 60
 tcc cgc ctc acc aac caa acc gtt gag gat ttg gaa aac cgc atc gct 599
 Ser Arg Leu Thr Asn Pro Thr Val Gln Ala Leu Glu Asn Arg Ile Ala
 65 70 75
 tcc ctc gaa ggt ggc gtc cac gct gta ggc ttc tcc tcc gga cag gcc 647
 Ser Leu Glu Gly Gly Val His Ala Val Ala Phe Ser Ser Gly Gln Ala
 80 85 90 95
 gca acc acc aac gtc att ttg aac ctg gca gga ggc ggc gac cac atc 695
 Ala Thr Thr Asn Ala Ile Leu Asn Leu Ala Gly Ala Gly Asp His Ile
 100 105 110
 gtc acc tcc cca cgc ctc tac ggt ggc acc gag act cta ttc ctt atc 743
 Val Thr Ser Pro Arg Leu Tyr Gly Gly Thr Gln Thr Leu Phe Leu Ile
 115 120 125
 act ctt aac cgc ctg ggt atc gat gtt tcc ttc gtg gaa aac ccc gac 791
 Thr Leu Asn Arg Leu Gly Ile Asp Val Ser Phe Val Glu Asn Pro Asp
 130 135 140
 gac cct gag tcc tgg cag gca gcc gtt cag cca aac acc aaa gca ttc 839
 Asp Pro Glu Ser Trp Gln Ala Ala Val Gln Pro Asn Thr Lys Ala Phe
 145 150 155
 ttc ggc gag act ttc gcc aac cca cag gca gac gtc ctg gat att cct 887
 Phe Gly Glu Thr Phe Ala Asn Pro Gln Ala Asp Val Leu Asp Ile Pro
 160 165 170 175
 gcg gtg gct gaa gtt gcg cac cgc aac agc gtt cca ctg atc atc gac 935
 Ala Val Ala Glu Val Ala His Arg Asn Ser Val Pro Leu Ile Ile Asp
 180 185 190
 aac acc atc gct acc gca gcg ctc gtg cgc ccg ctc gag ctc ggc gca 983
 Asn Thr Ile Ala Thr Ala Ala Leu Val Arg Pro Leu Glu Leu Gly Ala
 195 200 205
 gac gtt gtc gtc gct tcc ctc acc aag ttc tac acc ggc aac ggc tcc 1031
 Asp Val Val Val Ala Ser Leu Thr Lys Phe Tyr Thr Gly Asn Gly Ser
 210 215 220

gga ctg ggc ggc gtg ctt atc gac ggc gga aag ttc gat tgg act gtc 1079
 Gly Leu Gly Gly Val Leu Ile Asp Gly Gly Lys Phe Asp Trp Thr Val
 225 230 235

gaa aag gat gga aag cca gta ttc ccc tac ttc gtc act cca gat gct 1127
 Glu Lys Asp Gly Lys Pro Val Phe Pro Tyr Phe Val Thr Pro Asp Ala
 240 245 250 255

gct tac cag gga ttc aag tac gca gat ctt ggt gca cca gcc ttc ggc 1175
 Ala Tyr His Gly Leu Lys Tyr Ala Asp Leu Gly Ala Pro Ala Phe Gly
 260 265 270

ctg aag gtt cgc gtc ggc ctt cta cgc gac acc gcc tcc acc ctg tcc 1223
 Leu Lys Val Arg Val Gly Leu Leu Arg Asp Thr Gly Ser Thr Leu Ser
 275 280 285

gca ttc aac gca tgg gct gca gtc cag gcc atc gac acc ctt tcc ctg 1271
 Ala Phe Asn Ala Trp Ala Ala Val Gln Gly Ile Asp Thr Leu Ser Leu
 290 295 300

ccc ctg gag ccc ccc aac gaa aac gcc atc aag gtt gca gaa ttc ctg 1319
 Arg Leu Glu Arg His Asn Glu Asn Ala Ile Lys Val Ala Glu Phe Leu
 315 310 315

aac aac cag gag aag ctg gaa aag gtt aac ttc gca gcc ctg aag gat 1367
 Asn Asn His Glu Lys Val Glu Lys Val Asn Phe Ala Gly Leu Lys Asp
 320 325 330 335

tcc cct tgg tac gca acc aag gaa aag ctt gcc ctg aag tac acc gcc 1415
 Ser Pro Trp Tyr Ala Thr Lys Glu Lys Leu Gly Leu Lys Tyr Thr Gly
 340 345 350

tcc ctt ctg acc ttc gag atc aag gcc gcc aag gat gag gct tgg gca 1463
 Ser Val Leu Thr Phe Glu Ile Lys Gly Gly Lys Asp Glu Ala Trp Ala
 355 360 365

ttt atc gac gcc ctg aag cta ccc tcc aac ctt gca aac atc ggc gat 1511
 Phe Ile Asp Ala Leu Lys Leu His Ser Asn Leu Ala Asn Ile Gly Asp
 370 375 380

gtt gcc tcc ctg gtt gtt ccc cca gca acc acc acc cat tca gag tcc 1559
 Val Arg Ser Leu Val Val His Pro Ala Thr Thr Thr His Ser Glu Ser
 385 390 395

gac gaa gct gcc ctg gca cgc gcc gcc gtt acc cag tcc acc gtc cgc 1607
 Asp Glu Ala Gly Leu Ala Arg Ala Gly Val Thr Gln Ser Thr Val Arg
 400 405 410 415

ctg tcc gtt gcc atc gag acc att gat gat atc atc gct pac ctg gaa 1655
 Leu Ser Val Gly Ile Gln Thr Ile Asp Asp Ile Ile Ala Asp Leu Glu
 420 425 430

gcc gcc ttt gct gca atc tag ctttaaatag actcacccca gtgctt aag 1706
 Gly Gly Phe Ala Ala Ile
 435

cgcctgggttt ttctttttcca gactcgtgag aatgcaaaact agactagaca gagctgtcca 1765

tatacaattgg aagaagtittt agtcttgtcc acccagaaca gccggttatt ttcatgccca 1826

cctcgcgcc ttca 1840

02100: 2
 02110: 437
 02120: PBT
 02130: Corynebacterium glutamicum

04000: 2
 Met Pro Lys Tyr Asp Asn Ser Asn Ala Asp Gln Trp Gly Phe Glu Thr
 1 5 10 15
 Arg Ser Ile His Ala Gly Gln Ser Val Asp Ala Gln Thr Ser Ala Arg
 20 25 30
 Asn Leu Pro Ile Tyr Gln Ser Thr Ala Phe Val Phe Asp Ser Ala Glu
 35 40 45
 His Ala Lys Gln Arg Phe Ala Leu Glu Asp Leu Gly Pro Val Tyr Ser
 50 55 60
 Arg Leu Thr Asn Pro Thr Val Glu Ala Leu Glu Asn Arg Ile Ala Ser
 65 70 75 80
 Leu Glu Gly Gly Val His Ala Val Ala Phe Ser Ser Gly Gln Ala Ala
 85 90 95
 Thr Thr Asn Ala Ile Leu Asn Leu Ala Gly Ala Gly Asp His Ile Val
 100 105 110
 Thr Ser Pro Arg Leu Tyr Gly Gly Thr Glu Thr Leu Phe Leu Ile Thr
 115 120 125
 Leu Asn Arg Leu Gly Ile Asp Val Ser Phe Val Glu Asn Pro Asp Asp
 130 135 140
 Pro Glu Ser Trp Gln Ala Ala Val Gln Pro Asn Thr Lys Ala Phe Phe
 145 150 155 160
 Gly Glu Thr Phe Ala Asn Pro Gln Ala Asp Val Leu Asp Ile Pro Ala
 165 170 175
 Val Ala Glu Val Ala His Arg Asn Ser Val Pro Leu Ile Ile Asp Asn
 180 185 190
 Thr Ile Ala Thr Ala Ala Leu Val Arg Pro Leu Glu Leu Gly Ala Asp
 195 200 205
 Val Val Val Ala Ser Leu Thr Lys Phe Tyr Thr Gly Asn Gly Ser Gly
 210 215 220
 Leu Gly Gly Val Leu Ile Asp Gly Gly Lys Phe Asp Trp Thr Val Glu
 225 230 235 240
 Lys Asp Gly Lys Pro Val Phe Pro Tyr Phe Val Thr Pro Asp Ala Ala
 245 250 255
 Tyr His Gly Leu Lys Tyr Ala Asp Leu Gly Ala Pro Ala Phe Gly Leu
 260 265 270
 Lys Val Arg Val Gly Leu Leu Arg Asp Thr Gly Ser Thr Leu Ser Ala
 275 280 285

Phe Asn Ala Trp Ala Ala Val Gln Gly Ile Asp Thr Leu Ser Leu Arg
290 295 300

Leu Glu Arg His Asn Glu Asn Ala Ile Lys Val Ala Glu Phe Leu Asn
305 310 315 320

Asn His Glu Lys Val Glu Lys Val Asn Phe Ala Gly Leu Lys Asp Ser
325 330 335

Pro Trp Tyr Ala Thr Lys Glu Lys Leu Gly Leu Lys Tyr Thr Gly Ser
340 345 350

Val Leu Thr Phe Glu Ile Lys Gly Gly Lys Asp Glu Ala Trp Ala Phe
355 360 365

Ile Asp Ala Leu Lys Leu His Ser Asn Leu Ala Asn Ile Gly Asp Val
370 375 380

Arg Ser Leu Val Val His Pro Ala Thr Thr Thr His Ser Gln Ser Asp
385 390 395 400

Glu Ala Gly Leu Ala Arg Ala Gly Val Thr Gln Ser Thr Val Arg Leu
405 410 415

Ser Val Gly Ile Glu Thr Ile Asp Asp Ile Ile Ala Asp Leu Glu Gly
420 425 430

Gly Phe Ala Ala Ile
435

1110 3

1110 1495

1110 DNA

1110 Corynebacterium glutamicum

11200

11200 CDS

11200 (1267)..(1264)

1100 3

caatggttcc cccaggggaa acggtcttgg tattagcaact ttcacccgaa cagcctgcaa 60

gaatggcgac ggctaacagg gctgggattg tcccaactt cacttcgggc tctttcttag 120

caataggttc gtagaaaagt ttactagcct agagagtatg cgatttcttg aactggaaga 180

attgaagaat cgcgggacct tgaaatggac ccggtttcca gaagacgtgc ttcctttgtg 240

gggttgggaa agtgattttg gcacctgccc gcagttgaag gaagct atg gca gat 295
Met Ala Asp

1

gca gtt gag cgc gag gtc ttc gga tac cca cca gat gct act ggg ttg 343
Ala Val Glu Arg Glu Val Phe Gly Tyr Pro Pro Asp Ala Thr Gly Leu

5

10

15

aa: gat cgc ttg act gga ttc tac gag cgt cgc tat ggg ttt ggc cca 391
Asn Asp Ala Leu Thr Gly Phe Tyr Glu Arg Arg Tyr Gly Phe Gly Pro

20

25

30

35

aat cgg gaa agt gtt ttc gcc att ccg gat gtg gtt cgt ggc ctg aag 439
 Asn Pro Glu Ser Val Phe Ala Ile Pro Asp Val Val Arg Gly Leu Lys
 40 41 50

ctt gcc att gag cat ttc act aag cct ggt tgg gcg atc att gtg cgg 487
 Leu Ala Ile Glu His Phe Thr Lys Pro Gly Ser Ala Ile Ile Val Pro
 55 60 65

ttg cct gca tac cct cct ttc att gag ttg cct aag gtt act ggt cgt 535
 Leu Pro Ala Tyr Pro Pro Phe Ile Glu Leu Pro Lys Val Thr Gly Arg
 70 75 80

cag gcg atc tac att gat gcg cat gag tac gat ttg aag gaa att gag 583
 Gln Ala Ile Tyr Ile Asp Ala His Glu Tyr Asp Leu Lys Glu Ile Glu
 85 90 95

aag gcc ttc ggt gac ggt ggt gga tca ctg ttg ttc tgg aat cca cag 631
 Lys Ala Phe Ala Asp Gly Ala Gly Ser Leu Leu Phe Cys Asn Pro His
 100 105 110 115

aac cca ctg gcc aag ggt ttc tct gaa gag tac atc cgc gag ctc acc 679
 Asn Pro Leu Gly Thr Val Phe Ser Glu Glu Tyr Ile Arg Glu Leu Thr
 120 125 130

gat att gcg ggt aag tac gat gcc ctc atc atc gtc gat gag atc cag 727
 Asp Ile Ala Ala Lys Tyr Asp Ala Arg Ile Ile Val Asp Glu Ile His
 135 140 145

cgg cca ctg gtt tat gaa gcc acc cat ggg gtt gct gtt ggt gtt tct 775
 Ala Pro Leu Val Tyr Glu Gly Thr His Val Val Ala Ala Gly Val Ser
 150 155 160

gag aac gtt gga aac act ttc atc acc atc acc gca act tct aag cgg 823
 Glu Asn Ala Ala Asn Thr Cys Ile Thr Ile Thr Ala Thr Ser Lys Ala
 165 170 175

ttg aac act ggt ggt ttg aag tat gct cag atc ttc ttc agt aat gaa 871
 Trp Asn Thr Ala Gly Leu Lys Cys Ala Gln Ile Phe Phe Ser Asn Glu
 180 185 190 195

gcc gat ctg aag gcc ttg aag aat ttg tgg gat att acc cgt gac ggt 919
 Ala Asp Val Lys Ala Trp Lys Asn Leu Ser Asp Ile Thr Arg Asp Gly
 200 205 210

gtg tcc atc ctt gga ttg atc ggt cgg gag aca gtg tac aac gag ggc 967
 Val Ser Ile Leu Gly Leu Ile Ala Ala Glu Thr Val Tyr Asn Glu Gly
 215 220 225

gaa gaa ttc ctt gat gag tca att cag att ctc aag cac aac cgt gac 1015
 Glu Glu Phe Leu Asp Glu Ser Ile Gln Ile Leu Lys Asp Asn Arg Asp
 230 235 240

ttt gcg gct gct gaa ctg gaa aag ctt ggc gtg aag gtc ttc gaa cgg 1063
 Phe Ala Ala Ala Glu Leu Glu Lys Leu Gly Val Lys Val Tyr Ala Pro
 245 250 255

cac tcc act tat ttg atg tgg ttg gac ttc cct ggc acc aag atc gaa 1111
 Asp Ser Thr Tyr Leu Met Trp Leu Asp Phe Ala Gly Thr Lys Ile Glu
 260 265 270 275

gag ggc cct tct aaa att ctt cgt gag gag ggt aag gtc atg ctg aat 1159
 Glu Ala Pro Ser Lys Ile Leu Arg Glu Glu Gly Lys Val Met Leu Asn
 280 285 290

gat ggc gca gct ttt ggt ggt ttc acc acc tgc gct cgt ctt aat ttt 1207
 Asp Gly Ala Ala Phe Gly Gly Phe Thr Thr Cys Ala Arg Leu Asn Phe
 295 300 305

gag tct acc aga gag acc ctt gag gag ggg ctg cgc cgt atc gcc agc 1255
 Ala Cys Ser Arg Glu Thr Leu Glu Glu Gly Leu Arg Arg Ile Ala Ser
 310 315 320

gtg tgg taa ataagagta aaaagtctgt cctgattact tctttgatgc 1304
 Val Leu
 325

tgttttccat gtttttcgga gctggaaaacc tcatcttccc gccgatgctt ggattgtcgg 1364

caggaacaaa ctatctacca gctatctttag gattttctaga aacgagtggt ctgctccggg 1424

tcttggaat tatcgccggg gtgtttctcg gagaaantgt caaggacatg gctttctcgtg 1484

gcggtaaatc 1495

<21> 4

<211> 315

<212> F&T

<213> Corynebacterium glutanicum

<400> 4

Met Ala Asp Ala Val Glu Arg Glu Val Phe Gly Tyr Pro Pro Asp Ala
 1 5 10 15

Thr Gly Leu Asn Asp Ala Leu Thr Gly Phe Tyr Glu Arg Arg Tyr Gly
 20 25 30

Phe Gly Pro Asn Pro Glu Ser Val Phe Ala Ile Pro Asp Val Val Arg
 35 40 45

Gly Ser Lys Leu Ala Ile Glu His Phe Thr Lys Pro Gly Ser Ala Ile
 50 55 60

Ile Val Pro Leu Pro Ala Tyr Pro Pro Phe Ile Glu Leu Pro Lys Val
 65 70 75 80

Thr Gly Arg Gln Ala Ile Tyr Ile Asp Ala His Glu Tyr Asp Leu Lys
 85 90 95

Glu Ile Glu Lys Ala Phe Ala Asp Gly Ala Gly Ser Leu Leu Phe Cys
 100 105 110

Asn Pro His Asn Pro Leu Gly Thr Val Phe Ser Glu Glu Tyr Ile Arg
 115 120 125

Glu Leu Thr Asp Ile Ala Ala Lys Tyr Asp Ala Arg Ile Ile Val Asp
 130 135 140

Glu Ile His Ala Pro Leu Val Tyr Glu Gly Thr His Val Val Ala Ala
 145 150 155 160

Gly Val Ser Glu Asn Ala Ala Asn Thr Cys Ile Thr Ile Thr Ala Thr
165 170 175

Ser Lys Ala Trp Asn Thr Ala Gly Leu Lys Cys Ala Gln Ile Phe Phe
180 185 190

Ser Asn Glu Ala Asp Val Lys Ala Trp Lys Asn Leu Ser Asp Ile Thr
195 200 205

Arg Asp Gly Val Ser Ile Leu Gly Leu Ile Ala Ala Glu Thr Val Tyr
210 215 220

Asn Glu Gly Glu Glu Phe Leu Asp Glu Ser Ile Gln Ile Leu Lys Asp
225 230 235 240

Asn Arg Asp Phe Ala Ala Ala Glu Leu Glu Lys Leu Gly Val Lys Val
245 250 255

Tyr Ala Pro Asp Ser Thr Tyr Leu Met Trp Leu Asp Phe Ala Gly Thr
260 265 270

Lys Ile Glu Glu Ala Pro Ser Lys Ile Leu Arg Glu Glu Gly Lys Val
275 280 285

Met Leu Asn Asp Gly Ala Ala Phe Gly Gly Phe Thr Thr Cys Ala Arg
290 295 300

Leu Asn Phe Ala Cys Ser Arg Glu Thr Leu Glu Glu Gly Leu Arg Arg
305 310 315 320

Ile Ala Ser Val Leu
325

<210> 5

<211> 1033

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1006)

<400> 5

gtggcgatcg ggtatccgag ctacacttag aggtgttaga gatcatgagt ttccacgaac 60

tgtaacgcag gattcaccac tcaatgaaag gtcgaccgac atg agc act gaa gac 115
Met Ser Thr Glu Asp
1 5

att gtc gtc gta gca gta gat ggc tcg gac gcc tca aaa caa gct gtt 163
Ile Val Val Val Ala Val Asp Gly Ser Asp Ala Ser Lys Gln Ala Val
10 15 20

ggg tgg gct gca aat acc gcc aac aaa cgt ggc att cca ctt cgc ttg 211
Arg Trp Ala Ala Asn Thr Ala Asn Lys Arg Gly Ile Pro Leu Arg Leu
25 30 35

gct tcc agc tac acc atg cct cag ttc ctc tac gca gag gga atg gtt 259
Ala Ser Ser Tyr Thr Met Pro Gln Phe Leu Tyr Ala Glu Gly Met Val
40 45 50

cca cca caa gag ctt ttc gat gac ctc cag gcc gaa gcc ctg gaa aag	307
Pro Pro Gln Glu Leu Phe Asp Asp Leu Gln Ala Glu Ala Leu Glu Lys	
55 60 65	
att aac gaa gcc cgt gac atc gcc cat gag gta gcg cca gaa atc aag	355
Ile Asn Glu Ala Arg Asp Ile Ala His Glu Val Ala Pro Glu Ile Lys	
70 75 80 85	
atc ggg caa acc atc gct gaa ggc agt ccc atc gac atg ctg ttg gaa	403
Ile Gly His Thr Ile Ala Glu Gly Ser Pro Ile Asp Met Leu Leu Glu	
90 95 100	
atg tct ccc gat gcc aca atg atc gtc atg ggt tcc cgc gga ctc ggc	451
Met Ser Pro Asp Ala Thr Met Ile Val Met Gly Ser Arg Gly Leu Gly	
105 110 115	
gga ctc tcc gga atg gtc atc ggc tcc gtc tcc ggt gca atc atc agc	499
Gly Leu Ser Gly Met Val Met Gly Ser Val Ser Gly Ala Val Val Ser	
120 125 130	
aac gca aag tgt cca gtc gtt gtt gtc agt gaa gac agc gca gtc aac	547
His Ala Lys Cys Pro Val Val Val Val Arg Glu Asp Ser Ala Val Asn	
135 140 145	
gaa gac agc aag tac agt cca gtc gtc gtc agt gta gat tgt tcc gaa	595
Glu Asp Ser Lys Tyr Gly Pro Val Val Val Gly Val Asp Gly Ser Glu	
150 155 160 165	
gtc tcc aca aag gca acc gaa tac gca ttt gcg gaa gct gaa gct agt	643
Val Ser Gln Gln Ala Thr Glu Tyr Ala Phe Ala Glu Ala Glu Ala Arg	
170 175 180	
ggc gcc gaa ctc gtt gca gtt cac acc tgg atg gac atg cag gta cag	691
Gly Ala Glu Leu Val Ala Val His Thr Trp Met Asp Met Gln Val Gln	
185 190 195	
gca tca ctt gca ggt ctt gca gct gct caa cag cag tgg gat gaa gta	739
Ala Ser Leu Ala Gly Leu Ala Ala Gln Gln Gln Trp Asp Glu Val	
200 205 210	
gaa cgt cag caa acc gac atg ctg atc gaa cgc ctc gca cca ctg gta	787
Glu Arg Gln Gln Thr Asp Met Leu Ile Glu Arg Leu Ala Pro Leu Val	
215 220 225	
gaa aag tac cca agt gta acc gtc aag aag atc atc acc cgt gac cgc	835
Glu Lys Tyr Pro Ser Val Thr Val Lys Lys Ile Ile Thr Arg Asp Arg	
230 235 240 245	
cca gtt cgc gca ctt gca gaa gca tct gaa aac gcg cag ctc cta gtc	883
Pro Val Arg Ala Leu Ala Glu Ala Ser Glu Asn Ala Gln Leu Leu Val	
250 255 260	
gtt ggt tcc cat ggt cgt ggc gga ttt aag ggc atg ctc ctt ggc tcc	931
Val Gly Ser His Gly Arg Gly Gly Phe Lys Gly Met Leu Leu Gly Ser	
265 270 275	
acc tcc cgc gca ctg ctg caa tcc gca cng tgc cca atg atg gta gtt	979
Thr Ser Arg Ala Leu Leu Gln Ser Ala Pro Cys Pro Met Met Val Val	
280 285 290	

cgc cca cct gag aag att aag aag tag tttcttttaa gtttcgatgc cccgggtt 1033
 Arg Pro Pro Glu Lys Ile Lys Lys
 295 300

<210> 6

<211> 301

<212> PRT

<213> Corynebacterium glutamicum

<400> 6

Met Ser Thr Glu Asp Ile Val Val Val Ala Val Asp Gly Ser Asp Ala
 1 5 10 15

Ser Lys Gln Ala Val Arg Trp Ala Ala Asn Thr Ala Asn Lys Arg Gly
 20 25 30

Ile Pro Leu Arg Leu Ala Ser Ser Tyr Thr Met Pro Gln Phe Leu Tyr
 35 40 45

Ala Glu Gly Met Val Pro Pro Gln Glu Leu Phe Asp Asp Leu Gln Ala
 50 55 60

Glu Ala Leu Glu Lys Ile Asn Glu Ala Arg Asp Ile Ala His Glu Val
 65 70 75 80

Ala Pro Glu Ile Lys Ile Gly His Thr Ile Ala Glu Gly Ser Pro Ile
 85 90 95

Asp Met Leu Leu Glu Met Ser Pro Asp Ala Thr Met Ile Val Met Gly
 100 105 110

Ser Arg Gly Leu Gly Gly Leu Ser Gly Met Val Met Gly Ser Val Ser
 115 120 125

Gly Ala Val Val Ser His Ala Lys Cys Pro Val Val Val Val Arg Glu
 130 135 140

Asp Ser Ala Val Asn Glu Asp Ser Lys Tyr Gly Pro Val Val Val Gly
 145 150 155 160

Val Asp Gly Ser Glu Val Ser Gln Gln Ala Thr Glu Tyr Ala Phe Ala
 165 170 175

Glu Ala Glu Ala Arg Gly Ala Glu Leu Val Ala Val His Thr Trp Met
 180 185 190

Asp Met Gln Val Gln Ala Ser Leu Ala Gly Leu Ala Ala Ala Gln Gln
 195 200 205

Gln Trp Asp Glu Val Glu Arg Gln Gln Thr Asp Met Leu Ile Glu Arg
 210 215 220

Leu Ala Pro Leu Val Glu Lys Tyr Pro Ser Val Thr Val Lys Lys Ile
 225 230 235 240

Ile Thr Arg Asp Arg Pro Val Arg Ala Leu Ala Glu Ala Ser Glu Asn
 245 250 255

Ala Gln Leu Leu Val Val Gly Ser His Gly Arg Gly Gly Phe Lys Gly
 260 265 270

Met Leu Leu Gly Ser Thr Ser Arg Ala Leu Leu Gln Ser Ala Pro Cys
275 280 285

Pro Met Met Val Val Arg Pro Pro Glu Lys Ile Lys Lys
290 295 300

4210: -
4211: 948
4212: DNA
4213: Corynebacterium glutamicum

4220: -
4221: CD3
4222: 101 11 1925
4223: EXA00239

4400: -
gtggtttcaa cagagaccac cgggtgtgctt ggggtgacgc ctctggcgat cccaccgcac 60

tggtttgga gttttgggt ctacaatagc gaggggtgaat ttg acc atc ccc ttt 115
Leu Thr Ile Pro Phe
1 5

ggc aag ggc cac gcc acc gaa aac gac ttc atc atc atc ccc gat gag 163
Ala Lys Gly His Ala Thr Glu Asn Asp Phe Ile Ile Ile Pro Asp Glu
10 15 20

gat ccc gcc caa gat tta act cca gaa atg gtg gtc acg ctg tgt gac 211
Asp Ala Arg Leu Asp Leu Thr Pro Glu Met Val Val Thr Leu Cys Asp
25 30 35

ggc gcc gcc ggg atc ggt ggt gat ggt atc ctc cgc gtc gtt aaa ggt 259
Arg Arg Ala Gly Ile Gly Ala Asp Gly Ile Leu Arg Val Val Lys Ala
40 45 50

gga cac gta gaa gcc tcc acg gtc gac cca tgc ctg tgt ttc atg gat 307
Ala Asp Val Gln Gly Ser Thr Val Asp Pro Ser Leu Trp Phe Met Asp
55 60 65

tac gcc aac gcc gat gga cct ttg ggt gaa atg tgc ggc aat ggt gtg 355
Tyr Arg Asn Ala Asp Gly Ser Leu Ala Gln Met Cys Gly Asn Gly Val
70 75 80 85

ggc ctg ttc ggc cac tgg ctg tac tcc cgc ggt ctt gta gat aat acg 403
Arg Leu Phe Ala His Trp Leu Tyr Ser Arg Gly Leu Val Asp Asn Thr
90 95 100

agg ttt gat atc ggt acc ggc gac ggt gtc cgc cac gtt gat att ttg 451
Ser Phe Asp Ile Gly Thr Arg Ala Gly Val Arg His Val Asp Ile Leu
105 110 115

cag gca gat caa cat tct ggc cag gtc cgc gtt gat atg ggc atc cct 499
Gln Ala Asp Gln His Ser Ala Gln Val Arg Val Asp Met Gly Ile Pro
120 125 130

gac gtc acg gga tta tcc acc tgc gac atc aac ggc caa gta ttc ggt 547
Asp Val Thr Gly Leu Ser Thr Cys Asp Ile Asn Gly Gln Val Phe Ala
135 140 145

BGI-121CP2-11-1925-EXA00239

Leu Val Asp Asn Thr Ser Phe Asp Ile Gly Thr Arg Ala Gly Val Arg
100 105 110

His Val Asp Ile Leu Gln Ala Asp Gln His Ser Ala Gln Val Arg Val
 115 120 125
 Asp Met Gly Ile Pro Asp Val Thr Gly Leu Ser Thr Cys Asp Ile Asn
 130 135 140
 Gly Gln Val Phe Ala Gly Leu Gly Val Asp Met Gly Asn Pro His Leu
 145 150 155 160
 Ala Cys Val Val Pro Gly Leu Ser Ala Ser Ala Leu Ala Asp Met Glu
 165 170 175
 Leu Arg Ala Pro Thr Phe Asp Gln Glu Phe Phe Pro His Gly Val Asn
 180 185 190
 Val Glu Ile Val Thr Gln Leu Glu Asp Asp Ala Val Ser Met Arg Val
 195 200 205
 Trp Glu Arg Gly Val Gly Glu Thr Arg Ser Cys Gly Thr Gly Thr Val
 210 215 220
 Ala Ala Ala Cys Ala Ala Leu Ala Asp Ala Gly Leu Gly Glu Gly Thr
 225 230 235 240
 Ala Cys Val Cys Val Pro Arg Gly Glu Val Glu Val Gln Ile Phe Asp
 245 250 255
 Asp Gly Ser Thr Leu Thr Gly Pro Ser Ala Ile Ile Ala Leu Gly Glu
 260 265 270
 Val Gln Ile
 275

Q110 - 9
 Q111 - 1491
 Q112 - DNA
 Q113 - Corynebacterium glutamicum

Q110 -
 Q111 - CDS
 Q112 - (101)..(146?)
 Q113 - EXS02970

Q110 - 9
 aacgcgaaaa acagccgttc acgtgctaaa gcagctcggc ttgatctagg gtgaggtgag 60
 ttttttaag atttcataat attttgggga gtgaactggt ttg gca ttg aag ggt 115
 Leu Ala Leu Lys Gly
 1 5
 tac acc aac ttt gac ggt gaa ttc atc gaa ttc gga tct gtg caa gca 163
 Tyr Thr Asn Phe Asp Gly Glu Phe Ile Glu Phe Gly Ser Val Gln Ala
 10 15 20
 aaa gaa gag gaa aaa cgg gca ttc gac aac gat cgc gcg cac gtt ttc 211
 Lys Glu Glu Glu Lys Arg Ala Phe Asp Asn Asp Arg Ala His Val Phe
 25 30 35
 cac tcc tgg tcc gcg cag gac aaa atc agc ccc aaa gta tgg gca gct 259

His Ser Trp Ser Ala Gln Asp Lys Ile Ser Pro Lys Val Trp Ala Ala
4 45 50

gac gaa ggt tcc acg ctg tac gac ttc gac ggc aac ggc ttc atc gac 307
Ala Gln Gly Ser Thr Leu Tyr Asp Phe Asp Gly Asn Ala Phe Ile Asp
55 60 65

atg ggt tcc caa ctt gtc tgg gaa aac tta ggc cac aac aac cct cga 315
Met Gly Ser Gln Leu Val Ser Ala Asn Leu Gly His Asn Asn Pro Arg
70 75 80 85

tta gtc gag ggc atc cag cgc cca gca ggc cgg ttg aac aac atc aac 403
Leu Val Gln Ala Ile Gln Arg Gln Ala Ala Arg Leu Thr Asn Ile Asn
90 95 100

cag gac ttc ggc aat gat ggc cgc tct gat gtc gtc gaa aag atc gtc 451
Pro Ala Phe Gly Asn Asp Val Arg Ser Asp Val Ala Ala Lys Ile Val
105 110 115

tgg atg ggc cgt ggc gaa ttc ttc cac ggc ttt ttc aac aac ggc ggc 499
Ser Met Ala Arg Gly Glu Phe Ser His Val Phe Phe Thr Asn Gly Gly
120 125 130

gac gac ggc atc gag cac tcc atc cgc atg gct cgc ctg cac aac gga 547
Ala Asp Ala Ile Glu His Ser Ile Arg Met Ala Arg Leu His Thr Gly
135 140 145

cgc aac aaa atc ctg tcc gca ttc cgc agc tac cac ggc gca aac gga 595
Arg Asn Lys Ile Leu Ser Ala Tyr Arg Ser Tyr His Gly Ala Thr Gly
150 155 160 165

tcc ggc atg atg ctg acc ggc gaa cac cgc cgc ctg ggc aac cgc acc 643
Ser Ala Met Met Leu Thr Gly Glu His Arg Arg Leu Gly Asn Pro Thr
170 175 180

acc gac cca gct atc tac cac ttc tgg gca cca ttc ctg cac cca tcc 691
Thr Asp Pro Asp Ile Tyr His Phe Trp Ala Pro Phe Leu His His Ser
185 190 195

tca ttc ttt ggc acc acc caa gaa gaa gaa tcc gaa cgc gca ctg aag 739
Ser Phe Phe Ala Thr Thr Gln Glu Glu Glu Cys Glu Arg Ala Leu Lys
200 205 210

cac ttg gaa gat gtc atc cgc ttt gaa ggt gct ggc atg atc gaa ggc 787
His Leu Glu Asp Val Ile Ala Phe Glu Gly Ala Gly Met Ile Ala Ala
215 220 225

atc gtc ctg gag cca gtg gtg gga tca tca gga atc atc ctg cca cca 835
Ile Val Leu Glu Pro Val Val Gly Ser Ser Gly Ile Ile Leu Pro Pro
230 235 240 245

gca ggt tac tta aat ggc gtg ggc gaa ttt tgc aac aag cac gtc atc 883
Ala Gly Tyr Leu Asn Gly Val Arg Glu Leu Cys Asn Lys His Gly Ile
250 255 260

ctc ttc atc ggc gac gaa gtc atg gtc gga ttc gga ggc acc gaa aaa 931
Leu Phe Ile Ala Asp Glu Val Met Val Gly Phe Gly Arg Thr Gly Lys
265 270 275

ctg ttt gct tac gag cat gct ggc gac gat ttc cag cca gac atg atc 979
Leu Phe Ala Tyr Glu His Ala Gly Asp Asp Phe Gln Pro Asp Met Ile

280 285 290

acc ttc gcc aag ggt gtt aac gca ggt tac gcc cca ctg ggt ggc atc 1027
 Thr Phe Ala Lys Gly Val Asn Ala Gly Tyr Ala Pro Leu Gly Gly Ile
 295 300 305

gtg atg acc caa tca atc cgc gat acc ttc gga tca gag gca tac tcc 1075
 Val Met Thr Gln Ser Ile Arg Asp Thr Phe Gly Ser Glu Ala Tyr Ser
 310 315 320 325

ggc gga ctg acc tac tcc gga cag cca ctt gca gta gca ccc gcc aag 1123
 Gly Gly Leu Thr Tyr Ser Gly His Pro Leu Ala Val Ala Pro Ala Lys
 330 335 340

gca gcc ctg gag att tac gcc gaa gga gag atc att cca cgc gta gct 1171
 Ala Ala Leu Glu Ile Tyr Ala Glu Gly Glu Ile Ile Pro Arg Val Ala
 345 350 355

gca ctt gcc act gaa ctg atc gaa cct cgc ctt cgt gaa cta gcc gaa 1219
 Arg Leu Gly Ala Glu Leu Ile Glu Pro Arg Leu Arg Glu Leu Ala Glu
 360 365 370

gaa aac gta acc atc gct gac gtg cgg gcc atc gga ttc ttc tgg gaa 1267
 Glu Asn Val Ala Ile Ala Asp Val Arg Gly Ile Gly Phe Phe Trp Ala
 375 380 385

ctg gac ttc aat gca cag gcc act gcc atg gct gcc cgt gct gca gaa 1315
 Val Glu Phe Asn Ala Asp Ala Thr Ala Met Ala Ala Gly Ala Ala Glu
 390 395 400 405

ttc aag gaa cgc gcc gtg tgg ccg atg atc tcc ggc aac cga ttc cag 1363
 Phe Lys Glu Arg Gly Val Trp Pro Met Ile Ser Gly Asn Arg Phe His
 410 415 420

atc gcc cgg cgg ctg acc acc act gat gac gaa ttg gta gca ctg ctg 1411
 Ile Ala Pro Pro Leu Thr Thr Thr Asp Asp Glu Leu Val Ala Leu Leu
 425 430 435

gac cgg ctg gaa gct gca gcc caa gct gtc gag ctg acc ttc gct ggg 1459
 Asp Ala Val Glu Ala Ala Ala Gln Ala Val Glu Leu Thr Phe Ala Gly
 440 445 450

ccg ttg ttc taagttttct agataacaag gcc 1491
 Ala Leu Phe
 455

0109-10

0111-456

0121-PFT

0113-Corynebacterium glutamicum

0109-10

Leu Ala Leu Lys Gly Tyr Thr Asn Phe Asp Gly Glu Phe Ile Glu Phe
 1 5 10 15

Gly Ser Val Gln Ala Lys Glu Glu Glu Lys Arg Ala Phe Asp Asn Asp
 20 25 30

Arg Ala His Val Phe His Ser Trp Ser Ala Gln Asp Lys Ile Ser Pro
 35 40 45

Lys	Val	Trp	Ala	Ala	Ala	Glu	Gly	Ser	Thr	Leu	Tyr	Asp	Phe	Asp	Gly
50						55					60				
Asn	Ala	Phe	Ile	Asp	Met	Gly	Ser	Gln	Leu	Val	Ser	Ala	Asn	Leu	Gly
65					70					75					80
His	Asn	Asn	Pro	Arg	Leu	Val	Gln	Ala	Ile	Gln	Arg	Gln	Ala	Ala	Arg
				85					90					95	
Leu	Thr	Asn	Ile	Asn	Pro	Ala	Phe	Gly	Asn	Asp	Val	Arg	Ser	Asp	Val
			100					105					110		
Ala	Ala	Lys	Ile	Val	Ser	Met	Ala	Arg	Gly	Glu	Phe	Ser	His	Val	Phe
		115					120					125			
Phe	Thr	Asn	Gly	Gly	Ala	Asp	Ala	Ile	Gln	His	Ser	Ile	Arg	Met	Ala
130						135					140				
Arg	Leu	His	Thr	Gly	Arg	Asn	Lys	Ile	Leu	Ser	Ala	Tyr	Arg	Ser	Tyr
145					150					155					160
His	Gly	Ala	Thr	Gly	Ser	Ala	Met	Met	Leu	Thr	Gly	Glu	His	Arg	Arg
				165					170					175	
Leu	Gly	Asn	Pro	Thr	Thr	Asp	Pro	Asp	Ile	Tyr	His	Phe	Trp	Ala	Pro
			180					185					190		
Phe	Leu	His	His	Ser	Ser	Phe	Phe	Ala	Thr	Thr	Gln	Glu	Glu	Glu	Cys
	195						200					205			
Glu	Arg	Ala	Leu	Lys	His	Leu	Gln	Asp	Val	Ile	Ala	Phe	Gln	Gly	Ala
	210					215					220				
Gly	Met	Ile	Ala	Ala	Ile	Val	Leu	Glu	Pro	Val	Val	Gly	Ser	Ser	Gly
225					230					235					240
Ile	Ile	Leu	Pro	Pro	Ala	Gly	Tyr	Leu	Asn	Gly	Val	Arg	Glu	Leu	Cys
			245					250						255	
Asn	Lys	His	Gly	Ile	Leu	Phe	Ile	Ala	Asp	Glu	Val	Met	Val	Gly	Phe
		260						265					270		
Gly	Arg	Thr	Gly	Lys	Leu	Phe	Ala	Tyr	Gln	His	Ala	Gly	Asp	Asp	Phe
	275						280					285			
Gln	Pro	Asp	Met	Ile	Thr	Phe	Ala	Lys	Gly	Val	Asn	Ala	Gly	Tyr	Ala
	290					295					300				
Pro	Leu	Gly	Gly	Ile	Val	Met	Thr	Gln	Ser	Ile	Arg	Asp	Thr	Phe	Gly
				305						310					315
Ser	Glu	Ala	Tyr	Ser	Gly	Gly	Leu	Thr	Tyr	Ser	Gly	His	Pro	Leu	Ala
				320					325				330		
Val	Ala	Pro	Asa	Lys	Ala	Ala	Leu	Glu	Ile	Tyr	Ala	Glu	Gly	Glu	Ile
			340					345					350		
Ile	Pro	Arg	Val	Ala	Arg	Leu	Gly	Ala	Glu	Leu	Ile	Glu	Pro	Arg	Leu
	355						360					365			

Arg Glu Leu Ala Glu Glu Asn Val Ala Ile Ala Asp Val Arg Gly Ile
370 375 380

Gly Phe Phe Trp Ala Val Glu Phe Asn Ala Asp Ala Thr Ala Met Ala
385 390 395 400

Ala Gly Ala Ala Glu Phe Lys Glu Arg Gly Val Trp Pro Met Ile Ser
405 410 415

Gly Asn Arg Phe His Ile Ala Pro Pro Leu Thr Thr Thr Asp Asp Glu
420 425 430

Leu Val Ala Leu Leu Asp Ala Val Glu Ala Ala Ala Gln Ala Val Glu
435 440 445

Leu Thr Phe Ala Gly Ala Leu Phe
450 455

<210> 11
<211> 1330
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (131)...(1330)
<223> FRXA01009

<400> 11
aacccgacaaa acagccggttc acgtgctaaa gcagctcggc ttgatctagg gtgaggtgag 60

taataaaag acctataaat attctgggga gtaaacctgt tta gca ttg aag ggt 115
Leu Ala Leu Lys Gly
1 5

tac acc aac ttt gac ggt gaa ttc atc gaa ttc gga tot gtg caa gca 163
Tyr Thr Asn Phe Asp Gly Glu Phe Ile Glu Phe Gly Ser Val Gln Ala
10 15 20

aaa gaa gag gaa aaa cgg gca ttc gac aac gat cgc gcg cac gtt ttc 211
Lys Glu Glu Glu Lys Arg Ala Phe Asp Asn Asp Arg Ala His Val Phe
25 30 35

cac tcc tgg tcc gcg cag gac aaa atc agc ccc aaa gta tgg gca gct 259
His Ser Trp Ser Ala Gln Asp Lys Ile Ser Pro Lys Val Trp Ala Ala
40 45 50

gcc gaa ggt tcc acg ctg tac gac ttc gac ggc aac gcc ttc atc gac 307
Ala Glu Gly Ser Thr Leu Tyr Asp Phe Asp Gly Asn Ala Phe Ile Asp
55 60 65

atg ggt tcc caa ctt gtc tgg gca aac tta ggc cac aac aac cct cga 355
Met Gly Ser Gln Leu Val Ser Ala Asn Leu Gly His Asn Asn Pro Arg
70 75 80 85

tta gtt gag gcg atc cag cgc caa gca gcc cgg ttg acc aac atc aac 403
Leu Val Glu Ala Ile Gln Arg Gln Ala Ala Arg Leu Thr Asn Ile Asn
90 95 100

cag gcc ttc ggc aat gat gtg cgc tct gat gtt gct gca aag atc gtg 451

Pro	Ala	Phe	Gly	Asn	Asp	Val	Arg	Ser	Asp	Val	Ala	Ala	Lys	Ile	Val		
			105					110					115				
tcg	atg	gac	cgt	ggc	gaa	ttc	tcg	caa	gtg	ttt	ttc	acc	aac	ggc	ggc	499	
Ser	Met	Ala	Arg	Gly	Glu	Phe	Ser	His	Val	Phe	Phe	Thr	Asn	Gly	Gly		
		120					125					130					
gac	gac	gac	atc	gag	cac	tcg	atc	cgc	atg	gat	cgc	ctg	cac	acc	gga	547	
Ala	Asp	Ala	Ile	Glu	His	Ser	Ile	Arg	Met	Ala	Arg	Leu	His	Thr	Gly		
	135					140					145						
cgc	aac	aaa	att	ctg	tcg	gca	tac	cgc	agc	tac	caa	ggc	gca	acc	gga	595	
Arg	Asn	Lys	Ile	Leu	Ser	Ala	Tyr	Arg	Ser	Tyr	His	Gly	Ala	Thr	Gly		
150					155				160					165			
tcg	ggg	arg	atg	ctc	acc	ggc	gaa	caa	cgc	cgc	ctg	ggc	aac	ccc	acc	543	
Ser	Ala	Met	Met	Leu	Thr	Gly	Glu	His	Arg	Arg	Leu	Gly	Asn	Pro	Thr		
				170					175					18			
acc	gac	caa	gat	atc	tac	cac	ttc	tgc	gca	caa	ttc	ctg	cac	caa	tcg	591	
Thr	Asp	Pro	Asp	Ile	Tyr	His	Phe	Trp	Ala	Pro	Phe	Leu	His	His	Ser		
			185					190					195				
caa	ttc	ttc	gac	acc	acc	caa	gaa	gaa	gaa	tgc	gaa	cgc	gca	ctc	aag	739	
Ser	Phe	Phe	Ala	Thr	Thr	Glu	Glu	Glu	Glu	Cys	Glu	Arg	Ala	Leu	Lys		
	200					205					210						
caa	ctg	gaa	gat	gtc	atc	ggc	ctc	gaa	ggt	gat	ggc	atg	atc	gaa	gag	787	
His	Leu	Glu	Asp	Val	Ile	Ala	Phe	Glu	Gly	Ala	Gly	Met	Ile	Ala	Ala		
	15				220					22							
atc	acc	ctg	gag	cca	gag	gag	gaa	cca	caa	gga	atc	acc	ctg	cca	cca	855	
Ile	Val	Leu	Glu	Pro	Val	Val	Gly	Ser	Ser	Gly	Ile	Ile	Leu	Pro	Pro		
230				235						240				245			
gca	ggt	tac	tta	aat	cgc	ctg	ccc	gaa	ctt	tgc	aat	aag	cac	gga	atc	883	
Ala	Gly	Tyr	Leu	Asn	Gly	Val	Arg	Glu	Leu	Cys	Asn	Lys	His	Gly	Ile		
				250					255					260			
ctc	ttc	atc	gac	gac	gaa	gtc	atg	gtc	gga	ttc	gga	cgc	acc	gga	aaa	951	
Leu	Phe	Ile	Ala	Asp	Glu	Val	Met	Val	Gly	Phe	Gly	Arg	Thr	Gly	Lys		
		265						270					275				
ctg	ttc	gat	tac	caa	cat	gat	ggc	gac	gat	ttc	caa	cca	gac	atc	atc	979	
Leu	Phe	Ala	Tyr	Glu	His	Ala	Gly	Asp	Asp	Phe	Glu	Pro	Asp	Met	Ile		
		280					285					290					
acc	ttc	gac	aag	cgt	gtt	aac	gca	ggt	tac	gac	cca	ctc	ggt	ggc	atc	1027	
Thr	Phe	Ala	Lys	Gly	Val	Asn	Ala	Gly	Tyr	Ala	Pro	Leu	Gly	Gly	Ile		
	295					300					305						
gtg	atg	acc	caa	tca	atc	cgc	gat	acc	ttc	gga	tca	gag	gca	tac	tcg	1075	
Val	Met	Thr	Glu	Ser	Ile	Arg	Asp	Thr	Phe	Gly	Ser	Glu	Ala	Tyr	Ser		
310					315					320				325			
ggc	gga	ctc	acc	tac	tcg	gga	cac	cca	ctt	gca	gta	gca	ccc	ggc	aag	1123	
Gly	Gly	Leu	Thr	Tyr	Ser	Gly	His	Pro	Leu	Ala	Val	Ala	Pro	Ala	Lys		
			330					335					340				
gca	gca	ctg	gag	att	tac	ggc	gaa	gga	gag	atc	att	cca	cgc	gta	gct	1171	
Ala	Ala	Leu	Glu	Ile	Tyr	Ala	Glu	Gly	Glu	Ile	Ile	Pro	Arg	Val	Ala		

345	350	355	
aga ctt ggc gct gaa ctg atc gaa cct cgc ctt cgt gaa cta ggc gaa			1219
Arg Leu Gly Ala Glu Leu Ile Glu Pro Arg Leu Arg Glu Leu Ala Glu			
360	365	370	
gaa aac gta ggc atc gct gac gtg cgg ggc atc gga ttc ttc tgg gca			1267
Glu Asn Val Ala Ile Ala Asp Val Arg Gly Ile Gly Phe Phe Trp Ala			
375	380	385	
gtg gag ttc aat gca gac gcc act ggc atg gct gcc ggt gct gca gaa			1315
Val Glu Phe Asn Ala Asp Ala Thr Ala Met Ala Ala Gly Ala Ala Glu			
390	395	400	405
ttc aag gaa cgc ggc			1330
Phe Lys Glu Arg Gly			
410			

<210> 12
 <211> 410
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 12	
Leu Ala Leu Lys Gly Tyr Thr Asn Phe Asp Gly Glu Phe Ile Glu Phe	
1	10
Gly Ser Val Gln Ala Lys Glu Glu Glu Lys Arg Ala Phe Asp Asn Asp	
20	30
Arg Ala His Val Phe His Ser Trp Ser Ala Gln Asp Lys Ile Ser Pro	
35	45
Lys Val Trp Ala Ala Ala Glu Gly Ser Thr Leu Tyr Asp Phe Asp Gly	
50	60
Asn Ala Phe Ile Asp Met Gly Ser Gln Leu Val Ser Ala Asn Leu Gly	
65	75
His Asn Asn Pro Arg Leu Val Glu Ala Ile Gln Arg Gln Ala Ala Arg	
85	95
Leu Thr Asn Ile Asn Pro Ala Phe Gly Asn Asp Val Arg Ser Asp Val	
100	110
Ala Ala Lys Ile Val Ser Met Ala Arg Gly Glu Phe Ser His Val Phe	
115	125
Phe Thr Asn Gly Gly Ala Asp Ala Ile Glu His Ser Ile Arg Met Ala	
130	140
Arg Leu His Thr Gly Arg Asn Lys Ile Leu Ser Ala Tyr Arg Ser Tyr	
145	155
His Gly Ala Thr Gly Ser Ala Met Met Leu Thr Gly Glu His Arg Arg	
165	175
Leu Gly Asn Pro Thr Thr Asp Pro Asp Ile Tyr His Phe Trp Ala Pro	
180	190

Phe Leu His His Ser Ser Phe Phe Ala Thr Thr Gln Glu Glu Glu Cys
 195 200 205
 Glu Arg Ala Leu Lys His Leu Glu Asp Val Ile Ala Phe Glu Gly Ala
 210 215 220
 Gly Met Ile Ala Ala Ile Val Leu Glu Pro Val Val Gly Ser Ser Gly
 225 230 235 240
 Ile Ile Leu Pro Pro Ala Gly Tyr Leu Asn Gly Val Arg Glu Leu Cys
 245 250 255
 Asn Lys His Gly Ile Leu Phe Ile Ala Asp Glu Val Met Val Gly Phe
 260 265 270
 Gly Arg Thr Gly Lys Leu Phe Ala Tyr Glu His Ala Gly Asp Asp Phe
 275 280 285
 Glu Pro Asp Met Ile Thr Phe Ala Lys Gly Val Asn Ala Gly Tyr Ala
 290 295 300
 Pro Leu Gly Gly Ile Val Met Thr Gln Ser Ile Arg Asp Thr Phe Gly
 305 310 315 320
 Ser Glu Ala Tyr Ser Gly Gly Leu Thr Tyr Ser Gly His Pro Leu Ala
 325 330 335
 Val Ala Pro Ala Lys Ala Ala Leu Glu Ile Tyr Ala Glu Gly Glu Ile
 340 345 350
 Ile Pro Arg Val Ala Arg Leu Gly Ala Glu Leu Ile Glu Pro Arg Leu
 355 360 365
 Arg Glu Leu Ala Glu Glu Asn Val Ala Ile Ala Asp Val Arg Gly Ile
 370 375 380
 Gly Phe Phe Trp Ala Val Glu Phe Asn Ala Asp Ala Thr Ala Met Ala
 385 390 395 400
 Ala Gly Ala Ala Glu Phe Lys Glu Arg Gly
 405 410

<110> 13
 <111> 792
 <112> INA
 <113> Corynebacterium glutamicum

<110>
 <111> CDS
 <112> (101)..(769)
 <113> EXC02390

<400> 13
 gctgtgtgtg ctgaccata cgttggaaact ccaactgtg ttgataccgc caagatgttt 60
 ggcgcgaggg atctgttagc togtttogag tcataggagg gtg gag tgg acc gct 115
 Val Glu Trp Thr Ala
 1 5
 ttt ggc acc ctg att ctg ctc aat ttg gtg ggc agt tta tcc ccg ggg 163

Phe Gly Thr Leu Ile Leu Leu Asn Leu Val Gly Ser Leu Ser Pro Gly
 10 15 20
 cct gat acc ttt ttc ctg ctg cgc tta gcc acc cgc tcc aga gcg cac 211
 Pro Asp Thr Phe Leu Leu Arg Leu Ala Thr Arg Ser Arg Ala His
 25 30 35
 ggg atc gct ggg gtc gcc ggc atc gtc acc gga ctg acg gtg tgg gtg 259
 Ala Ile Ala Gly Val Ala Gly Ile Val Thr Gly Leu Thr Val Trp Val
 40 45 50
 acg ctg acg gta gtg gga gga ggc gcc ctg ctg acc act tat cag tag 307
 Thr Leu Thr Val Val Gly Ala Ala Ala Leu Leu Thr Thr Tyr Pro Ser
 55 60 65
 att ctg gga atc atc caa ctg gtc gcc gcc acc tac cta agc ttc att 355
 Ile Leu Gly Ile Ile Gln Leu Val Gly Gly Thr Tyr Leu Ser Phe Ile
 70 75 80
 ggg tac aag ttc ctg cgc tcc gcc tcc aga gag ctt atc gac gcc cgc 403
 Gly Tyr Lys Leu Leu Arg Ser Ala Ser Arg Gln Leu Ile Asp Ala Arg
 85 90 95 100
 cag ttc cgt ttc aac gcc tat gcc cga cct att ccc gat gcc gta gaa 451
 Gln Phe Arg Phe Asn Ala Asp Ala Arg Pro Ile Pro Asp Ala Val Glu
 105 110 115
 gaa ctg gga acc cgc act cag gta tat cca caa ggt ttg gcc acc aac 499
 Ala Leu Gly Thr Arg Thr Gln Val Tyr Arg Gln Gly Leu Ala Thr Asn
 120 125 130
 ctg tca aac cct aaa gtt ttc atg tac ttc gcc gcc acc ctg gct ccc 547
 Leu Ser Asn Pro Lys Val Val Met Tyr Phe Ala Ala Ile Leu Ala Pro
 135 140 145
 tgg atg cca ggc cag cca tca ccc gta ctg gcc ttc tcc acc atc gta 595
 Leu Met Pro Ala His Pro Ser Pro Val Leu Ala Phe Ser Ile Ile Val
 150 155 160 165
 gag att tta gtc cag acc ttt gtt acc ttc tcc gct gtg cgc ctg att 643
 Ala Ile Leu Val Gln Thr Phe Val Thr Phe Ser Ala Val Cys Leu Ile
 170 175 180
 gcc tcc acc gag cgt gtc cgc aaa gcc atg ctg cgt gcc ggt ccc tgg 691
 Val Ser Thr Glu Arg Val Arg Lys Ala Met Leu Arg Ala Gly Pro Trp
 185 190 195
 ttt cag ctg ctt gct gcc att gtc ttc ctg att gtg ggt gtg act ctg 739
 Phe Asp Leu Leu Ala Gly Val Val Phe Leu Val Val Gly Val Thr Leu
 200 205 210
 ctg tat gaa gcc ctg acc ggt tta ctg ggg taaaggcata aaaaatggct 789
 Leu Tyr Glu Gly Leu Thr Gly Leu Leu Gly
 215 220
 tcc 792

<110> 14
 <111> 223
 <112> PRT

<213> Corynebacterium glutamicum

<400> 14

Val Glu Trp Thr Ala Phe Gly Thr Leu Ile Leu Leu Asn Leu Val Gly
1 5 10 15

Ser Leu Ser Pro Gly Pro Asp Thr Phe Phe Leu Leu Arg Leu Ala Thr
20 25 30

Arg Ser Arg Ala His Ala Ile Ala Gly Val Ala Gly Ile Val Thr Gly
35 40 45

Ile Thr Val Trp Val Thr Leu Thr Val Val Gly Ala Ala Ala Leu Leu
50 55 60

Thr Thr Tyr Pro Ser Ile Leu Gly Ile Ile Gln Leu Val Gly Gly Thr
65 70 75 80

Tyr Leu Ser Phe Ile Gly Tyr Lys Leu Leu Arg Ser Ala Ser Arg Gln
85 90 95

Ile Ile Asp Ala Arg Gln Phe Arg Phe Asn Ala Asp Ala Arg Pro Ile
10 105 110

Pro Asp Ala Val Glu Ala Leu Gly Thr Arg Thr Gln Val Tyr Arg Gln
115 120 125

Gly Leu Ala Thr Asn Leu Ser Asn Pro Lys Val Val Met Tyr Phe Ala
130 135 140

Ala Ile Leu Ala Pro Leu Met Pro Ala His Pro Ser Pro Val Leu Ala
145 150 155 160

Phe Ser Ile Ile Val Ala Ile Leu Val Gln Thr Phe Val Thr Phe Ser
165 170 175

Ala Val Cys Leu Ile Val Ser Thr Glu Arg Val Arg Lys Ala Met Leu
180 185 190

Arg Ala Gly Pro Trp Phe Asp Leu Leu Ala Gly Val Val Phe Leu Val
195 200 205

Val Gly Val Thr Leu Leu Tyr Gln Gly Leu Thr Gly Leu Leu Gly
210 215 220

<210> 15

<211> 197

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(374)

<223> EXCD1796

<400> 15

atgtaantcg atcaggtgga aatgcccgca aaagtggcgg cgggtggcga gggatggcgg 60

atgggtgggc atcgggtggc tgctactagt cgggctcttc ttg ctc ctt ggc ggt 115
Leu Leu Leu Gly Gly

	1	5	
aac cct gcc gag atc gac cag gtt tta ggt gcc gat caa acc cag atc			163
Asn. Pro Ala Glu Ile Asp Gln Val Leu Gly Gly Asp Gln Thr Gln Ile			
	10	20	
gag tct gga gag tcc acc gga gcc gcc gag ttt gat cac tcc caa acc			211
Glu Ser Gly Glu Ser Thr Gly Ala Gly Asp Phe Asp His Cys Gln Thr			
	25	30	35
ggc gca gat gcc aac gcc agt gat gat tgt cgc ctt tac tcc acc tca			259
Gly Ala Asp Ala Asn Ala Ser Asp Asp Cys Arg Leu Tyr Tyr Thr Ser			
	40	45	50
ctc tcc gtc aat gaa arg tgg cag act ttg ctt cca gct cag gct ggt			307
Phe Ser Val Asn Glu Met Trp Gln Thr Leu Leu Pro Ala Gln Ala Gly			
	55	60	65
atc gaa tac acc gag ccg acc ttg act ctt ttc aaa aac tcc acc caa			355
Ile Glu Tyr Thr Glu Pro Thr Leu Thr Leu Phe Lys Asn Ser Thr Gln			
	70	75	80
acc gcc tgc ggt ttc ggt tct gcc tcc act ggg ccg ttt tcc tgt ccg			403
Thr Gly Cys Gly Phe Ala Ser Ala Ser Thr Gly Pro Phe Tyr Cys Pro			
	90	95	100
tca gac caa gat gct tat ttg gac ttg act ttc tcc gat cag atg cgt			451
Ser Asp Gln Asp Ala Tyr Phe Asp Leu Thr Phe Phe Asp Gln Met Arg			
	105	110	115
cag ttc ggt gca gaa aac gct ccg ctt gcc cag arg tac atc gtg gcc			499
Gln Phe Gly Ala Glu Asn Ala Pro Leu Ala Gln Met Tyr Ile Val Ala			
	120	125	130
cac gag tac gcc cac cac gtc caa aac ctc gag ggc acc ctc gga ctg			547
His Glu Tyr Gly His His Val Gln Asn Leu Glu Gly Thr Leu Gly Leu			
	135	140	145
tcc aat tac aac gat ccg gcc gct gat tcc aac gcc gtc aag atc gag			595
Ser Asn Tyr Asn Asp Pro Gly Ala Asp Ser Asn Ala Val Lys Ile Glu			
	150	155	160
ttg cag gcc gat tgc tac gca gcc att tgg gct aat cac tcc acc gaa			643
Leu Gln Ala Asp Cys Tyr Ala Gly Ile Trp Ala Asn His Ser Ser Glu			
	170	175	180
ggc ccg gat ccg cta ctc caa ccc atc acc gaa tct gag cta gat tcc			691
Gly Pro Asp Pro Leu Leu Gln Pro Ile Thr Glu Ser Glu Leu Asp Ser			
	185	190	195
gct ttc ctt gct gca agc gcc gtg gcc gag gac aat atc cag caa cga			739
Ala Leu Leu Ala Ala Ser Ala Val Gly Asp Asp Asn Ile Gln Gln Arg			
	200	205	210
tcc ggt gcc gat gtc aat cct gaa agc tgg act cac gcc tca tgg cag			787
Ser Gly Gly Asp Val Asn Pro Glu Ser Trp Thr His Gly Ser Ser Gln			
	215	220	225
cag ccg aaa gac gcc ttc ctc gcc gcc tac aac acc gcc cag atg agc			835
Gln Arg Lys Asp Ala Phe Leu Ala Gly Tyr Asn Thr Gly Gln Met Ser			
	230	235	240
			245

tttttgcagc tct

897

<400>	16																
Leu	Leu	Leu	Gly	Gly	Asn	Pro	Ala	Glu	Ile	Asp	Gln	Val	Leu	Gly	Gly		
1				5					10					15			
Asp	Gln	Thr	Gln	Ile	Glu	Ser	Gly	Glu	Ser	Thr	Gly	Ala	Gly	Asp	Phe		
			20					25					30				
Asp	His	Cys	Gln	Thr	Gly	Ala	Asp	Ala	Asn	Ala	Ser	Asp	Asp	Cys	Arg		
		35					40					45					
Leu	Tyr	Tyr	Thr	Ser	Phe	Ser	Val	Asn	Glu	Met	Trp	Gln	Thr	Leu	Leu		
	50					55					60						
Pro	Ala	Gln	Ala	Gly	Ile	Glu	Tyr	Thr	Glu	Pro	Thr	Leu	Thr	Leu	Phe		
65					70					75					80		
Lys	Asn	Ser	Thr	Gln	Thr	Gly	Cys	Gly	Phe	Ala	Ser	Ala	Ser	Thr	Gly		
				85					90						95		
Pro	Phe	Tyr	Cys	Pro	Ser	Asp	Gln	Asp	Ala	Tyr	Phe	Asp	Leu	Thr	Phe		
			100					105					110				
Phe	Asp	Gln	Met	Arg	Gln	Phe	Gly	Ala	Glu	Asn	Ala	Pro	Leu	Ala	Gln		
		115					120					125					
Met	Tyr	Ile	Val	Ala	His	Glu	Tyr	Gly	His	His	Val	Gln	Asn	Leu	Glu		
	130					135					140						
Gly	Thr	Leu	Gly	Leu	Ser	Asn	Tyr	Asn	Asp	Pro	Gly	Ala	Asp	Ser	Asn		
145					150				155						160		
Ala	Val	Lys	Ile	Glu	Leu	Gln	Ala	Asp	Cys	Tyr	Ala	Gly	Ile	Trp	Ala		
			165						170					175			
Asn	His	Ser	Ser	Glu	Gly	Pro	Asp	Pro	Leu	Leu	Gln	Pro	Ile	Thr	Glu		
			180					185					190				
Ser	Gln	Leu	Asp	Ser	Ala	Leu	Leu	Ala	Ala	Ser	Ala	Val	Gly	Asp	Asp		
		195					200					205					
Asn	Ile	Gln	Gln	Arg	Ser	Gly	Gly	Asp	Val	Asn	Pro	Glu	Ser	Trp	Thr		
	210					215					220						
His	Gly	Ser	Ser	Gln	Gln	Arg	Lys	Asp	Ala	Phe	Leu	Ala	Gly	Tyr	Asn		
225					230					235					240		
Thr	Gly	Gln	Met	Ser	Ala	Cys	Asp	Phe	Leu	Gly	Arg	Gly	Val	Tyr	Asn		
				245					250					255			

Asp Ala

(210> 17
 (211> 771
 (212> DNA
 (213> Corynebacterium glutamicum

(220>
 (221> CDS
 (222> (101)..(748)
 (223> RXC01207

(400> 17
 atcatgata tcaacggcag agcgggtttt gttacagcgc gtaaaactgtg aatttgaaaa 60
 aattttaaac aatccgtaca ccaacttcag gagaaaaaca gtg agc aga atc tat 115
 Val Ser Arg Ile Tyr
 1 5
 gac tgt gcc gac caa gac tcc cgt gca gca gcc cta aag gag gct gtc 163
 Asp Cys Ala Asp Gln Asp Ser Arg Ala Ala Gly Leu Lys Ala Ala Val
 10 15 20
 tat gca gtc aaa att ggt cag ttc gcc gtc ttc ccc aag gat acc att 211
 Asp Ala Val Lys Ala Gly Gln Leu Val Val Leu Pro Thr Asp Thr Leu
 25 30 35
 tac gga ctc gcc tcc gac gct ttc aac aac cag gca gta gcc aac att 259
 Tyr Gly Leu Gly Cys Asp Ala Phe Asn Asn Glu Ala Val Ala Asn Leu
 40 45 50
 ctg gcc acc aaa cac cgt gcc ccc gat atg ccc gtt cca gtg ctc gtc 307
 Leu Ala Thr Lys His Arg Gly Pro Asp Met Pro Val Pro Val Leu Val
 55 60 65
 ggc agc tgg gac acc att caa gga ctt gtg cac tcc tat tct ggc cag 355
 Gly Ser Trp Asp Thr Ile Gln Gly Leu Val His Ser Tyr Ser Ala Gln
 70 75 80 85
 gca aaa ggc ctc gtg gag gcc ttc tgg cct ggt gga ctg tcc atc atc 403
 Ala Lys Ala Leu Val Glu Ala Phe Trp Pro Gly Gly Leu Ser Ile Ile
 90 95 100
 gtt ccg cag gca cca agc ctt ccg tgg aac ctt gcc gat acc cgt gcc 451
 Val Pro Gln Ala Pro Ser Leu Pro Trp Asn Leu Gly Asp Thr Arg Gly
 105 110 115
 acc gta atg ctg cgc atg cca ctg cac cca gtt gcc att gaa ttg ctg 499
 Thr Val Met Leu Arg Met Pro Leu His Pro Val Ala Ile Glu Leu Leu
 120 125 130
 cgc caa acc gga cca atg gct gtc tcc tcc gcc aac atc tcc gga cat 547
 Arg Gln Thr Gly Pro Met Ala Val Ser Ser Ala Asn Ile Ser Gly His
 135 140 145
 act cct cca acc acc gtg ctg gag gct cgt cag cag ctc aac caa aat 595
 Thr Pro Pro Thr Thr Val Leu Glu Ala Arg Gln Gln Leu Asn Glr Asn
 150 155 160 165

gtc ggt gtc tac ctc gat ggt ggc gaa tgc gag ctg gcc acc cat tca 643
 Val Ala Val Tyr Leu Asp Gly Gly Glu Cys Ala Leu Ala Thr Pro Ser
 170 175 180

acc atc gtg gat att tca ggc ccc gca cca aag att ttg cgt gag ggt 691
 Thr Ile Val Asp Ile Ser Gly Pro Ala Pro Lys Ile Leu Arg Glu Gly
 185 190 195

gcc atc agc gca gaa cgc gtt ggc gaa gta ctt gga gtg tcg gca gaa 739
 Ala Ile Ser Ala Glu Arg Val Gly Glu Val Leu Gly Val Ser Ala Glu
 200 205 210

agc ctg cgc taaatgggag tcggtttcgc ggg 771
 Ser Leu Arg
 215

<210> 18
 <211> 216
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 18
 Val Ser Arg Ile Tyr Asp Cys Ala Asp Gln Asp Ser Arg Ala Ala Gly
 1 5 10 15

Leu Lys Ala Ala Val Asp Ala Val Lys Ala Gly Gln Leu Val Val Leu
 20 25 30

Pro Thr Asp Thr Leu Tyr Gly Leu Gly Cys Asp Ala Phe Asn Asn Glu
 35 40 45

Ala Val Ala Asn Leu Leu Ala Thr Lys His Arg Gly Pro Asp Met Pro
 50 55 60

Val Pro Val Leu Val Gly Ser Trp Asp Thr Ile Gln Gly Leu Val His
 65 70 75 80

Ser Tyr Ser Ala Gln Ala Lys Ala Leu Val Glu Ala Phe Trp Pro Gly
 85 90 95

Gly Leu Ser Ile Ile Val Pro Gln Ala Pro Ser Leu Pro Trp Asn Leu
 100 105 110

Gly Asp Thr Arg Gly Thr Val Met Leu Arg Met Pro Leu His Pro Val
 115 120 125

Ala Ile Glu Leu Leu Arg Gln Thr Gly Pro Met Ala Val Ser Ser Ala
 130 135 140

Asn Ile Ser Gly His Thr Pro Pro Thr Thr Val Leu Glu Ala Arg Gln
 145 150 155 160

Gln Leu Asn Gln Asn Val Ala Val Tyr Leu Asp Gly Gly Glu Cys Ala
 165 170 175

Leu Ala Thr Pro Ser Thr Ile Val Asp Ile Ser Gly Pro Ala Pro Lys
 180 185 190

Ile Leu Arg Glu Gly Ala Ile Ser Ala Glu Arg Val Gly Glu Val Leu

205

gaa gac agc aag ttc ggc cca gtc gtc gtc ggt gtg gat ggc tcc gaa 595
Glu Asp Ser Lys Tyr Gly Pro Val Val Val Gly Val Asp Gly Ser Glu

150	155	160	165	
gtc tcc caa cag gca acc gaa tac gca ttt gcg gaa gct gaa gct cgt				643
Val Ser Gln Gln Ala Thr Glu Tyr Ala Phe Ala Glu Ala Glu Ala Arg				
170	175	180		
ggc ggc gaa ctc gtt gca gtt ctc acc tgg atg gac atg cag gta cag				691
Gly Ala Glu Leu Val Ala Val His Thr Trp Met Asp Met Gln Val Gln				
185	190	195		
gca tca ctt gca ggt ctt gca ggt gct caa cag cag tgg gat gaa gtg				739
Ala Ser Leu Ala Gly Leu Ala Ala Ala Gln Gln Gln Trp Asp Glu Val				
200	205	210		
gaa cgt cag caa acc gac atg ctg atc gaa cgc ctc gca cca ctg gtg				787
Glu Arg Gln Gln Thr Asp Met Leu Ile Glu Arg Leu Ala Pro Leu Val				
215	220	225		
gaa aag tac cca acc gta acc gtc aag aag atc atc acc cgt gac cgc				835
Glu Lys Tyr Pro Ser Val Thr Val Lys Lys Ile Ile Thr Arg Asp Arg				
230	235	240	245	
cca ctt cgc gca ctt gca gaa gca tct gaa aac gcg cag ctc cta gtc				883
Pro Val Arg Ala Leu Ala Glu Ala Ser Glu Asn Ala Gln Leu Leu Val				
250	255	260		
ctt cgt tcc cat gct cgt ggc gga ttt aag ggc atg ctc ctt ggc tcc				931
Val Gly Ser His Gly Arg Gly Gly Phe Lys Gly Met Leu Leu Gly Ser				
265	270	275		
acc tcc cgc gca ctg ctg caa tcc gca ccg tgc cca atg atg gtg gtt				979
Thr Ser Arg Ala Leu Leu Gln Ser Ala Pro Cys Pro Met Met Val Val				
280	285	290		
cgc cca cct gag aag att sag aag tagttttcttt taagtttoga tgc				1026
Arg Pro Pro Glu Lys Ile Lys Lys				
295	300			

-210- 20

-211- 301

-212- PET

-213- Corynebacterium glutamicum

-400- 20

Met Ser Thr Glu Asp Ile Val Val Val Ala Val Asp Gly Ser Asp Ala

1

5

10

15

Ser Lys Gln Ala Val Arg Trp Ala Ala Asn Thr Ala Asn Lys Arg Gly

20

25

30

Ile Pro Leu Arg Leu Ala Ser Ser Tyr Thr Met Pro Gln Phe Leu Tyr

35

40

45

Ala His Gly Met Val Pro Pro Gln Glu Leu Phe Asp Asp Leu Gln Ala

50

55

60

Glu Ala Leu Glu Lys Ile Asn Glu Ala Arg Asp Ile Ala His Glu Val

65

70

75

80

Ala Pro Glu Ile Lys Ile Gly His Thr Ile Ala Glu Gly Ser Pro Ile

85

90

95

Asp Met Leu Leu Glu Met Ser Pro Asp Ala Thr Met Ile Val Met Gly
 100 105 110

Ser Arg Gly Leu Gly Gly Leu Ser Gly Met Val Met Gly Ser Val Ser
 115 120 125

Gly Ala Val Val Ser His Ala Lys Cys Pro Val Val Val Val Arg Glu
 130 135 140

Asp Ser Ala Val Asn Glu Asp Ser Lys Tyr Gly Pro Val Val Val Gly
 145 150 155 160

Val Asp Gly Ser Glu Val Ser Gln Gln Ala Thr Glu Tyr Ala Phe Ala
 165 170 175

Glu Ala Glu Ala Arg Gly Ala Glu Leu Val Ala Val His Thr Trp Met
 180 185 190

Asp Met Gln Val Gln Ala Ser Leu Ala Gly Leu Ala Ala Ala Gln Gln
 195 200 205

Gln Trp Asp Glu Val Gln Arg Gln Gln Thr Asp Met Leu Ile Glu Arg
 210 215 220

Ile Ala Pro Leu Val Gln Lys Tyr Pro Ser Val Thr Val Lys Lys Ile
 225 230 235 240

Ile Thr Arg Asp Arg Pro Val Arg Ala Leu Ala Glu Ala Ser Glu Asn
 245 250 255

Ala Gln Leu Leu Val Val Gly Ser His Gly Arg Gly Gly Phe Lys Gly
 260 265 270

Met Leu Leu Gly Ser Thr Ser Arg Ala Leu Leu Gln Ser Ala Pro Cys
 275 280 285

Arg Met Met Val Val Arg Pro Pro Glu Lys Ile Lys Lys
 290 295 300

110 - 21
 111 - 1052
 112 - DNA
 113 - *Corynebacterium glutamicum*

1140 -
 111 - CDS
 1112 - (101)...(1036)
 1113 - FK200552

1140 - 21
 ccgcacacaa ggcagcaaaag ctgcacacaa ttgacgcctt gagttatgag taaaagctc 60

gtttttaagg tagcacacaa tcgcactaga ctgaagaact ggc gct acc tca aaa 115
 Val Ala Thr Ser Lys
 1 5

att ctt ctt tat tac gca ttc acc ccg ctc tct gac cct aaa gcg gtt 163
 Ile Leu Leu Tyr Tyr Ala Phe Thr Pro Leu Ser Asp Pro Lys Ala Val

10					15					20						
cag	ctg	tgg	cag	cgt	gag	ctc	tgc	gag	tca	ctg	aat	ctt	cgt	ggc	cgc	211
Gln	Leu	Trp	Gln	Arg	Glu	Leu	Cys	Glu	Ser	Leu	Asn	Leu	Arg	Gly	Arg	
25					30					35						
atc	ctg	atc	tcc	act	cac	ggc	acc	aat	gga	acc	gtg	ggc	gga	gat	att	259
Ile	Leu	Ile	Ser	Thr	His	Gly	Ile	Asn	Gly	Thr	Val	Gly	Gly	Asp	Ile	
40					45					50						
gat	gat	tgc	aag	gog	tac	att	aaa	aag	acc	cgc	gag	tac	cga	ggt	tcc	30
Asp	Asp	Cys	Lys	Ala	Tyr	Ile	Lys	Lys	Thr	Arg	Glu	Tyr	Pro	Gly	Phe	
55					60					65						
aac	cgc	atg	cag	ttt	aag	tgg	tcc	gag	ggt	ggc	gct	gag	gat	tcc	cga	355
Asn	Arg	Met	Gln	Phe	Lys	Trp	Ser	Glu	Gly	Gly	Ala	Glu	Asp	Pro	Pro	
70					75					80						
cag	ctc	agt	gtc	aaa	gtc	cac	gat	gag	atc	gtc	ggc	tcc	ggc	ggt	cga	400
Lys	Leu	Ser	Val	Lys	Val	Arg	Asp	Glu	Ile	Val	Ala	Phe	Gly	Ala	Pro	
90					95					100						
gat	gag	tcc	aaa	gtg	gtc	gaa	aac	ggc	gtc	gtc	ggg	ggc	ggc	ggt	cac	451
Asp	Glu	Leu	Lys	Val	Asp	Glu	Asn	Gly	Val	Val	Val	Gly	Gly	Val	His	
105					110					115						
ctg	aaa	cga	cag	cag	gtc	atc	gag	ctt	gtc	gaa	ggc	cgt	ggc	gat	gaa	499
Leu	Lys	Pro	Gln	Gln	Val	Asn	Glu	Leu	Val	Glu	Ala	Arg	Gly	Asp	Glu	
120					125					130						
gtt	gtg	tac	tcc	gac	gtc	cac	aac	gga	atg	gaa	ggc	cag	atc	ggc	aag	547
Val	Val	Phe	Phe	Asp	Gly	Arg	Asn	Ala	Met	Glu	Ala	Gln	Ile	Gly	Lys	
135					140					145						
tcc	aag	cac	gat	gtt	gtc	cct	gac	gta	gaa	acc	act	cac	gat	tcc	atc	595
Phe	Lys	Asp	Ala	Val	Val	Pro	Asp	Val	Glu	Thr	Thr	His	Asp	Pro	Ile	
150					155					160						
gga	gaa	atc	gag	tct	gga	aaa	tac	gac	gat	cct	aaa	gac	aag	cct	gtg	645
Ala	Glu	Ile	Glu	Ser	Gly	Lys	Tyr	Asp	Asp	Leu	Lys	Asp	Lys	Pro	Val	
170					175					180						
gtc	acc	tac	tcc	acc	ggc	gta	atc	cgt	cct	gac	atc	ctg	agt	tcc	ctc	691
Val	Thr	Tyr	Cys	Thr	Gly	Gly	Ile	Arg	Cys	Glu	Ile	Leu	Ser	Ser	Leu	
185					190					195						
atg	atc	aac	cct	ggc	tcc	aaa	gag	gtc	tac	cac	atc	gat	ggc	ggt	atc	739
Met	Ile	Asn	Arg	Gly	Phe	Lys	Glu	Val	Tyr	Gln	Ile	Asp	Gly	Gly	Ile	
200					205					210						
gtt	cgc	tac	ggc	gag	cag	ttt	ggc	aac	aag	ggc	ctg	tgg	gaa	ggt	tcc	787
Val	Arg	Tyr	Gly	Glu	Gln	Phe	Gly	Asn	Lys	Gly	Leu	Trp	Glu	Gly	Ser	
215					220					225						
ctc	tac	gtt	tcc	gat	aag	cgc	atg	cac	atg	gaa	tcc	ggc	gag	gat	tac	835
Leu	Tyr	Val	Phe	Asp	Lys	Arg	Met	His	Met	Glu	Phe	Gly	Glu	Asp	Tyr	
230					235					240						
aaa	gag	ctc	gga	cac	tcc	atc	cac	tcc	gat	act	cgc	acc	aac	aaa	ttt	883
Lys	Glu															

gag cac tgc ctc aac gaa gat gat tgc cgc gag ctc qtg ttg atg tgc 931
 Glu His Cys Leu Asn Glu Asp Asp Cys Arg Glu Leu Val Leu Met Cys
 265 270 275

cct gat tgc ttc gcc aat gtt gag acc cgt cat tgc aag cgc gaa cgc 979
 Pro Asp Cys Phe Ala Asn Val Glu Thr Arg His Cys Lys Arg Glu Arg
 280 285 290

tgt gca gca att gct ggc gat ttc gct gag gaa gga att gat ccg ctc 1027
 Cys Ala Ala Ile Ala Ala Asp Phe Ala Glu Gln Gly Ile Asp Pro Leu
 295 300 305

ggt act cct taaaaagggt atggtggctg ggt 1059
 Val Thr Ser
 310

G210> 12
 G211> 31:
 G212> PRT
 G213> Corynebacterium glutamicum

G400> 12
 Val Ala Thr Ser Lys Ile Leu Leu Tyr Tyr Ala Phe Thr Pro Leu Ser
 1 5 10 15

Asp Pro Lys Ala Val Gln Leu Trp Gln Arg Glu Leu Cys Glu Ser Leu
 20 25 30

Asn Leu Arg Gly Arg Ile Leu Ile Ser Thr His Gly Ile Asn Gly Thr
 35 40 45

Val Gly Gly Asp Ile Asp Asp Cys Lys Ala Tyr Ile Lys Lys Thr Arg
 50 55 60

Glu Tyr Pro Gly Phe Asn Arg Met Gln Phe Lys Trp Ser Glu Gly Gly
 65 70 75 80

Ala Gln Asp Phe Pro Lys Leu Ser Val Lys Val Arg Asp Glu Ile Val
 85 90 95

Ala Phe Gly Ala Pro Asp Glu Leu Lys Val Asp Gln Asn Gly Val Val
 100 105 110

Gly Gly Gly Val His Leu Lys Pro Gln Gln Val Asn Glu Leu Val Glu
 115 120 125

Ala Arg Gly Asp Glu Val Val Phe Phe Asp Gly Arg Asn Ala Met Glu
 130 135 140

Ala Gln Ile Gly Lys Phe Lys Asp Ala Val Val Pro Asp Val Gln Thr
 145 150 155 160

Thr His Asp Phe Ile Ala Glu Ile Gln Ser Gly Lys Tyr Asp Asp Leu
 165 170 175

Lys Asp Lys Pro Val Val Thr Tyr Cys Thr Gly Gly Ile Arg Cys Glu
 180 185 190

Ile Leu Ser Ser Leu Met Ile Asn Arg Gly Phe Lys Glu Val Tyr Gln

[illegible]

gag tcc ctt ggc gca gaa gcc caa tct ttc acg ggc tct cag gct ggt 402
 Glu Ser Leu Gly Ala Glu Ala Gln Ser Phe Thr Gly Ser Gln Ala Gly
 90 95 100

gta ctc acc acc gag cgc cac gga aac gca cgc att gtt gat gtc act 451
 Val Leu Thr Thr Glu Arg His Gly Asn Ala Arg Ile Val Asp Val Thr
 105 110 115

cca ggt cgt ggt cgt gaa gca ctc gat gag ggc aag atc tcc att gtt 499
 Pro Gly Arg Val Arg Glu Ala Leu Asp Glu Gly Lys Ile Cys Ile Val
 120 125 130

gct ggt tcc cag ggt gtt aat aaa gaa acc cgc gat gtc acc acg ttg 547
 Ala Gly Phe Gln Gly Val Asn Lys Glu Thr Arg Asp Val Thr Thr Leu
 135 140 145

ggt ctt ggt ggt tct cag acc act gca gtt ggc ttg gaa gct gct ttg 593
 Gly Arg Gly Gly Ser Asp Thr Thr Ala Val Ala Leu Ala Ala Ala Leu
 150 155 160 165

aac gct gat ggt tgt cag att tac tct gac gtt gac ggt ggt tat acc 643
 Asn Ala Asp Val Cys Glu Ile Tyr Ser Asp Val Asp Gly Val Tyr Thr
 170 175 180

gct gac cgc cgc atc ctt cct aat gca cag aag ctg gaa aag ctc acc 691
 Ala Asp Pro Arg Ile Val Pro Asn Ala Gln Lys Leu Glu Lys Leu Ser
 185 190 195

ttc gaa gaa atg ctg gaa ctt gct gct gtt ggc tcc aag att ttg ctg 739
 Ile Glu Glu Met Leu Glu Leu Ala Ala Val Gly Ser Lys Ile Leu Val
 200 205 210

ctg cgc agt ctt gaa cac gct cgt gca ttc aat gag cca ctt cgc gta 787
 Leu Arg Ser Val Glu Tyr Ala Arg Ala Phe Asn Val Pro Leu Arg Val
 215 220 225

cgc tct tct tat agt aat gat ccc ggc act ttg aat gcc ggc tct arg 835
 Arg Ser Ser Tyr Ser Asn Asp Pro Gly Thr Leu Ile Ala Gly Ser Met
 230 235 240 245

gag gat att ctt ggt gaa gaa gca gtc ctt acc ggt gtc gca acc gac 883
 Glu Asp Ile Pro Val Glu Glu Ala Val Leu Thr Gly Val Ala Thr Asp
 250 255 260

arg tcc gaa gcc aaa gta acc gtt ctg ggt att tcc gat aag cca ggc 931
 Lys Ser Glu Ala Lys Val Thr Val Leu Gly Ile Ser Asp Lys Pro Gly
 265 270 275

gag ctt jcg aag gtt ttc cgt ggc ttg gct gat gca gaa atc aac att 979
 Glu Ala Ala Lys Val Phe Arg Ala Leu Ala Asp Ala Glu Ile Asn Ile
 280 285 290

gac atg gtt cag cag aac gtc tct tct gta gaa gac ggc acc acc gac 1027
 Asp Met Val Leu Gln Asn Val Ser Ser Val Glu Asp Gly Thr Thr Asp
 295 300 305

atc acc ttc acc tgc cct cgt tcc gac ggc cgc cgc jcg atg gag atc 1075
 Ile Thr Phe Thr Cys Pro Arg Ser Asp Gly Arg Arg Ala Met Glu Ile
 310 315 320 325

ttg aag aag ctt cag gtt cag ggc aac tgg acc aat gtc ctt tac gac 1123

Leu Lys Lys Leu Gln Val Gln Gly Asn Trp Thr Asn Val Leu Tyr Asp
 330 335 340
 gag cag gtc ggc aaa gtc tcc ctg gtg ggt gct ggc atg aag tct cac 1171
 Asp Gln Val Gly Lys Val Ser Leu Val Gly Ala Gly Met Lys Ser His
 345 350 355
 cca ggt gtt acc gca gag ttc atg gaa gct ctg cgc gat gtc aac gtg 1219
 Pro Gly Val Thr Ala Glu Phe Met Glu Ala Leu Arg Asp Val Asn Val
 360 365 370
 aac atc gaa ttg att tcc acc tct gag att cgt att tcc gtg ctg atc 1267
 Asn Ile Glu Leu Ile Ser Thr Ser Glu Ile Arg Ile Ser Val Leu Ile
 375 380 385
 cgt gaa gat gat ctg gat gct gct gaa cgt gaa ttg cat gag cag ttc 1315
 Arg Glu Asp Asp Leu Asp Ala Ala Ala Arg Ala Leu His Glu Gln Phe
 390 395 400 405
 cag ttg ggc ggc gaa gac gaa gac gct gct tat gca ggc acc aga cgc 1363
 Gln Leu Gly Gly Glu Asp Glu Ala Val Val Tyr Ala Gly Thr Gly Arg
 410 415 420
 taaagtattt aagtagtagt ttt 1386

 <210> 24
 <211> 421
 <212> PRT
 <213> Corynebacterium glutamicum

 <400> 24
 Val Ala Leu Val Val Gln Lys Tyr Gly Gly Ser Ser Leu Glu Ser Ala
 1 5 10 15
 Glu Arg Ile Arg Asn Val Ala Glu Arg Ile Val Ala Thr Lys Lys Ala
 20 25 30
 Gly Asn Asp Val Val Val Val Cys Ser Ala Met Gly Asp Thr Thr Asp
 35 40 45
 Glu Leu Leu Glu Leu Ala Ala Ala Val Asn Pro Val Pro Pro Ala Arg
 50 55 60
 Glu Met Asp Met Leu Leu Thr Ala Gly Glu Arg Ile Ser Asn Ala Leu
 65 70 75 80
 Val Ala Met Ala Ile Glu Ser Leu Gly Ala Glu Ala Gln Ser Phe Thr
 85 90 95
 Gly Ser Gln Ala Gly Val Leu Thr Thr Glu Arg His Gly Asn Ala Arg
 100 105 110
 Ile Val Asp Val Thr Pro Gly Arg Val Arg Glu Ala Leu Asp Glu Gly
 115 120 125
 Lys Ile Cys Ile Val Ala Gly Phe Gln Gly Val Asn Lys Glu Thr Arg
 130 135 140
 Asp Val Thr Thr Leu Gly Arg Gly Gly Ser Asp Thr Thr Ala Val Ala
 145 150 155 160

Leu Ala Ala Ala Leu Asn Ala Asp Val Cys Glu Ile Tyr Ser Asp Val
 165 170 175
 Asp Gly Val Tyr Thr Ala Asp Pro Arg Ile Val Pro Asn Ala Gln Lys
 180 185 190
 Leu Gln Lys Leu Ser Phe Glu Glu Met Leu Glu Leu Ala Ala Val Gly
 195 200 205
 Ser Lys Ile Leu Val Leu Arg Ser Val Glu Tyr Ala Arg Ala Phe Asn
 210 215 220
 Val Pro Leu Arg Val Arg Ser Ser Tyr Ser Asn Asp Pro Gly Thr Leu
 225 230 235 240
 Ile Ala Gly Ser Met Glu Asp Ile Pro Val Glu Glu Ala Val Leu Thr
 245 250 255
 Gly Val Ala Phe Asp Lys Ser Glu Ala Lys Val Thr Val Leu Gly Ile
 260 265 270
 Ser Asp Lys Pro Gly Glu Ala Ala Lys Val Phe Arg Ala Leu Ala Asp
 275 280 285
 Ala Glu Ile Asn Ile Asp Met Val Leu Gln Asn Val Ser Ser Val Glu
 290 295 300
 Asp Gly Thr Thr Asp Ile Thr Phe Thr Cys Pro Arg Ser Asp Gly Arg
 305 310 315 320
 Arg Ala Met Glu Ile Leu Lys Lys Leu Gln Val Glu Gly Asn Thr Thr
 325 330 335
 Asn Val Leu Tyr Asp Asp Gln Val Gly Lys Val Ser Leu Val Gly Ala
 340 345 350
 Gly Met Lys Ser His Pro Gly Val Thr Ala Glu Phe Met Glu Ala Leu
 355 360 365
 Arg Asp Val Asn Val Asn Ile Glu Leu Ile Ser Thr Ser Glu Ile Arg
 370 375 380
 Ile Ser Val Leu Ile Arg Glu Asp Asp Leu Asp Ala Ala Ala Arg Ala
 385 390 395 400
 Leu His Glu Gln Phe Gln Leu Gly Gly Glu Asp Glu Ala Val Val Tyr
 405 410 415
 Ala Gly Thr Gly Arg
 420

(210) 15
 (211) 115a
 (212) DNA
 (213) *Corynebacterium glutamicum*

(210)
 (211) CDS
 (222) (101)..(1132)

42231 PXA-0533

04001 15

ctgcacgtgc attgcatgag cagttccagc tgggcggcga agacgaagcc gtcgtttatg 60

cagggacccg acgctaaaagt tttaaaggag tagttttaca atg acc acc atc gca 115
Met Thr Thr Ile Ala
1 5

att att ggt gca acc ggc cag gtc ggc cag gtt atg cgc acc ctt ttg 163
Val Val Gly Ala Thr Gly Gln Val Gly Gln Val Met Arg Thr Leu Leu
10 15 20

aaa gag cgc aat ttc cca gct gac act gtt cgt ttc ttt gct tcc cca 211
Glu Glu Arg Asn Phe Pro Ala Asp Thr Val Arg Phe Phe Ala Ser Pro
25 30 35

cgt tcc gca gcc cgt aag att gaa ttc cgt ggc acc gaa atc gag gta 259
Arg Ser Ala Gly Arg Lys Ile Glu Phe Arg Gly Thr Glu Ile Glu Val
40 45 50

aaa aac att act cag gca acc gag gag tcc ttc tag gac atc gac gtt 307
Glu Asp Ile Thr Gln Ala Thr Glu Glu Ser Leu Lys Asp Ile Asp Val
55 60 65

cgt ttc ttc tcc gct gga gcc acc gct tcc aag tag tcc gct cca ctg 355
Ala Leu Phe Ser Ala Gly Gly Thr Ala Ser Lys Gln Tyr Ala Pro Leu
70 75 80 85

ttc att ggt gca gcc gcc act gtt gtc gat aac ttc ttt gct tgg cgc 403
Phe Ala Ala Ala Gly Ala Thr Val Val Asp Asn Ser Ser Ala Trp Arg
90 95 100

aag aac gat gag gtt cca cca atc gtc tcc gag gtc aac cct tcc gac 451
Lys Asp Asp Glu Val Pro Leu Ile Val Ser Glu Val Asn Pro Ser Asp
105 110 115

tag gat ttc ctg gtc aag gcc att att gcc aac cct aac tgc acc acc 499
Lys Asp Ser Leu Val Lys Gly Ile Ile Ala Asn Pro Asn Cys Thr Thr
120 125 130

atg gct ggt atg cca gtc ctg aag cca ctt cag gat gca gct ggt ctt 547
Met Ala Ala Met Pro Val Leu Lys Pro Leu His Asp Ala Ala Gly Leu
135 140 145

gta aac ctt cag gtt tcc tct cag cag gct gtt tcc ggt tct ggt ctt 595
Val Lys Leu His Val Ser Ser Tyr Gln Ala Val Ser Gly Ser Gly Leu
150 155 160 165

gca ggt ggt gaa acc ctg gca aag cag gtt gct gca gtt gga gac cag 643
Ala Gly Val Glu Thr Leu Ala Lys Gln Val Ala Ala Val Gly Asp His
170 175 180

aac gtt gag ttc gtc cat gat gga cag gct gct gac gca gcc gat gtc 691
Asn Val Glu Phe Val His Asp Gly Gln Ala Ala Asp Ala Gly Asp Val
185 190 195

gga cct tat gtt tca cca atc gct tac aac gtc ctg cca ttc gcc gga 739
Gly Pro Tyr Val Ser Pro Ile Ala Tyr Asn Val Leu Pro Phe Ala Gly
200 205 210

115
163
211
259
307
355
403
451
499
547
595
643
691
739

aac ctc gtc gat gac ggc acc ttc gaa acc gat gaa gag cag aag ctg 757
 Asn Leu Val Asp Asp Gly Thr Phe Glu Thr Asp Glu Glu Gln Lys Leu
 215 220 225

ggc aac gaa tcc cgc aag att ctc ggt ctc cca gac ctc aag gtc tca 835
 Arg Asn Glu Ser Arg Lys Ile Leu Gly Leu Pro Asp Leu Lys Val Ser
 230 235 240 245

ggc acc tgc gtc cgc gtg cag gtt ttc acc ggt cag acg ctg acc att 883
 Gly Thr Cys Val Arg Val Pro Val Phe Thr Gly His Thr Leu Thr Ile
 250 255 260

cac gcc gaa ttc gac aag gca atc acc gtg gac cag gag cag gag atc 931
 His Ala Glu Phe Asp Lys Ala Ile Thr Val Asp Gln Ala Gln Glu Ile
 265 270 275

tig ggt gcc gct tca ggc gtc aag att gtc gac gtc cca acc cca att 979
 Leu Gly Ala Ala Ser Gly Val Lys Leu Val Asp Val Pro Thr Pro Leu
 280 285 290

gca gct gcc ggc att gac gaa tcc ctc gtt gga cgc atc cgt cag gac 1027
 Ala Ala Ala Gly Ile Asp Glu Ser Leu Val Gly Arg Ile Arg Gln Asp
 295 300 305

ccc act gtc gac gat aac cgc ggt ctg gtt ctc gtc gta tct ggc gac 1075
 Ser Thr Val Asp Asp Asn Arg Gly Leu Val Leu Val Val Ser Gly Asp
 310 315 320 325

aac ctc cgc aag ggt gct gag cta aac acc atc cag atc gct gag ctg 1123
 Asn Leu Arg Lys Gly Ala Ala Leu Asn Thr Ile Gln Ile Ala Glu Leu
 330 335 340

atg gtt aag taaaaacccg ccaataaaaa ctc 1155
 Leu Val Lys

<210> 26
 <211> 344
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 26
 Met Thr Thr Ile Ala Val Val Gly Ala Thr Gly Gln Val Gly Gln Val
 1 5 10 15

Met Arg Thr Leu Leu Glu Glu Arg Asn Phe Pro Ala Asp Thr Val Arg
 20 25 30

Phe Phe Ala Ser Pro Arg Ser Ala Gly Arg Lys Ile Glu Phe Arg Gly
 35 40 45

Thr Glu Ile Glu Val Glu Asp Ile Thr Gln Ala Thr Glu Glu Ser Leu
 50 55 60

Lys Asp Ile Asp Val Ala Leu Phe Ser Ala Gly Gly Thr Ala Ser Lys
 65 70 75 80

Gln Tyr Ala Pro Leu Phe Ala Ala Ala Gly Ala Thr Val Val Asp Asn
 85 90 95

Ser Ser Ala Trp Arg Lys Asp Asp Glu Val Pro Leu Ile Val Ser Glu
100 105 110

Val Asn Pro Ser Asp Lys Asp Ser Leu Val Lys Gly Ile Ile Ala Asn
115 120 125

Pro Asn Cys Thr Thr Met Ala Ala Met Pro Val Leu Lys Pro Leu His
130 135 140

Asp Ala Ala Gly Leu Val Lys Leu His Val Ser Ser Tyr Gln Ala Val
145 150 155 160

Ser Gly Ser Gly Leu Ala Gly Val Glu Thr Leu Ala Lys Gln Val Ala
165 170 175

Ala Val Gly Asp His Asn Val Glu Phe Val His Asp Gly Gln Ala Ala
180 185 190

Asp Ala Gly Asp Val Gly Pro Tyr Val Ser Pro Ile Ala Tyr Asn Val
195 200 205

Leu Pro Phe Ala Gly Asn Leu Val Asp Asp Gly Thr Phe Glu Thr Asp
210 215 220

Glu Glu Gln Lys Leu Arg Asn Glu Ser Arg Lys Ile Leu Gly Leu Pro
225 230 235 240

Asp Leu Lys Val Ser Gly Thr Cys Val Arg Val Pro Val Phe Thr Gly
245 250 255

His Thr Leu Thr Ile His Ala Glu Phe Asp Lys Ala Ile Thr Val Asp
260 265 270

Gln Ala Gln Glu Ile Leu Gly Ala Ala Ser Gly Val Lys Leu Val Asp
275 280 285

Val Pro Thr Pro Leu Ala Ala Ala Gly Ile Asp Glu Ser Leu Val Gly
290 295 300

Arg Ile Arg Gln Asp Ser Thr Val Asp Asp Asn Arg Gly Leu Val Leu
305 310 315 320

Val Val Ser Gly Asp Asn Leu Arg Lys Gly Ala Ala Leu Asn Thr Ile
325 330 335

Gln Ile Ala Glu Leu Leu Val Lys
340

4110-27

4110-508

4110-DNA

4110-Corynebacterium glutamicum

4210

4210-CHS

4210-(69)...(608)

4210-EXA0284

4400-27

cccattgcgc ggaggtcgca ccccttcgga cttgaactga taggcgcata gaaattattc 60

tggacgtc atg act act gct tcc gca acc gga att gca aca ctg acc tcc 110
Met Thr Thr Ala Ser Ala Thr Gly Ile Ala Thr Leu Thr Ser
1 5 10

acc ggc gac gtc ctg gac gtg tgg tat cca gaa atc ggg tcc acc gac 158
Thr Gly Asp Val Leu Asp Val Trp Tyr Pro Glu Ile Gly Ser Thr Asp
15 20 25 30

cag tcc gag ctg aca cct cta gaa ggc gtc gat gaa gat cga aac gtc 206
Gln Ser Ala Leu Thr Pro Leu Glu Gly Val Asp Glu Asp Arg Asn Val
35 40 45

acc ggc aaa atc gtg acg aca act atc gac acc gac gca gcc ccc acc 254
Thr Arg Lys Ile Val Thr Thr Thr Ile Asp Thr Asp Ala Ala Pro Thr
50 55 60

gac aac tac gat gaa tgg ctg cgc att ttc ctg ttc tac cag cgc gtt 302
Asp Thr Tyr Asp Ala Trp Leu Arg Leu His Leu Leu Ser His Arg Val
65 70 75

tta agc cct cag acc atc aac cta gac ggc att tta gac ctg ctg aac 350
Phe Arg Pro His Thr Ile Asn Leu Asp Gly Ile Phe Gly Leu Leu Asn
80 85 90

aat gtc gta tgg acc aac ttc gga cgc tat gca ttc gac ggt ttc gca 398
Asn Val Val Trp Thr Asn Phe Gly Pro Cys Ala Val Asp Gly Phe Ala
95 100 105 110

ctc acc cgc ggc cgc ctg tca cgc cga ggc caa gtt acc gtt tat agc 446
Leu Thr Arg Ala Arg Leu Ser Arg Arg Gly Gln Val Thr Val Tyr Ser
115 120 125

gtc gac aag ttc cca cgc atg gtc gac tat gtg gtt ccc tgg ggc gtg 494
Val Asp Lys Phe Pro Arg Met Val Asp Tyr Val Val Pro Ser Gly Val
130 135 140

cgc atc ggt gac gcc gac cgc gtc cga ctt ggc ggc tac ctg gca gat 542
Arg Ile Gly Asp Ala Asp Arg Val Arg Leu Gly Ala Tyr Leu Ala Asp
145 150 155

ggc acc acc gtg atg cat gag ggc ttc gtg aac ttc aac gct ggc acg 590
Gly Thr Thr Val Met His Glu Gly Phe Val Asn Phe Asn Ala Gly Thr
160 165 170

ctc ggc gct tcc atg gtt 608
Leu Gly Ala Ser Met Val
175 180

<210> 28

<211> 180

<212> PRT

<213> Corynebacterium glutamicum

<400> 28

Met Thr Thr Ala Ser Ala Thr Gly Ile Ala Thr Leu Thr Ser Thr Gly
1 5 10 15

Asp Val Leu Asp Val Trp Tyr Pro Glu Ile Gly Ser Thr Asp Gln Ser
20 25 30

Ala Leu Thr Pro Leu Glu Gly Val Asp Glu Asp Arg Asn Val Thr Arg
35 40 45

Lys Ile Val Thr Thr Thr Ile Asp Thr Asp Ala Ala Pro Thr Asp Thr
50 55 60

Tyr Asp Ala Trp Leu Arg Leu His Leu Leu Ser His Arg Val Phe Arg
65 70 75 80

Pro His Thr Ile Asn Leu Asp Gly Ile Phe Gly Leu Leu Asn Asn Val
85 90 95

Val Trp Thr Asn Phe Gly Pro Cys Ala Val Asp Gly Phe Ala Leu Thr
100 105 110

Arg Ala Arg Leu Ser Arg Arg Gly Gln Val Thr Val Tyr Ser Val Asp
115 120 125

Lys Phe Pro Arg Met Val Asp Tyr Val Val Pro Ser Gly Val Arg Ile
130 135 140

Gly Asp Ala Asp Arg Val Arg Leu Gly Ala Tyr Leu Ala Asp Gly Thr
145 150 155 160

Thr Val Met His His Gly Phe Val Asn Phe Asn Ala Gly Thr Leu Gly
165 170 175

Ala Ser Met Val
180

<210> 29
<211> 1230
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1207)
<223> RXA02022

<400> 29
tatattgggat tccaaatggt tgggtccgg gaattgtttt actaatttt taatcgagg 60

cttccatcat gttttaacta aggtttgtag gcttaaact gtg aac tct gaa ctc 115
Val Asn Ser Glu Leu
1 5

aaa cca gga tta gat ctc ctc ggc gac cca att gtc ctt act caa cgt 163
Lys Pro Gly Leu Asp Leu Leu Gly Asp Pro Ile Val Leu Thr Gln Arg
10 15 20

ttg gta gat ata cgg agt cgg tgg ggt cag gaa aag cag att got gat 211
Leu Val Asp Ile Pro Ser Pro Ser Gly Gln Glu Lys Gln Ile Ala Asp
25 30 35

gaa att gaa gat ggc ctt cgg aac ctt aat cta cct ggt gta gag gtc 259
Glu Ile Glu Asp Ala Leu Arg Asn Leu Asn Leu Pro Gly Val Glu Val
40 45 50

ttc cgc ttc aac aac aac gtt ctt ggt cgc acg aac agg gga ttg gcc	307
Phe Arg Phe Asn Asn Asn Val Leu Ala Arg Thr Asn Arg Gly Leu Ala	
55 60 65	
tcg agg gtc atg ctt ggt ggt cat atc gat aca gtg cgg atc gag gac	355
Ser Arg Val Met Leu Ala Gly His Ile Asp Thr Val Pro Ile Ala Asp	
70 75 80 85	
aat ctg cca agc cgt gtg gaa gac gcc atc atg tat gcc tgt gcc acc	403
Asn Leu Pro Ser Arg Val Glu Asp Gly Ile Met Tyr Gly Cys Gly Thr	
90 95 100	
gtc gat atg aaa tct ggg ttg ggg gtg tat ttg cat act ctt gcc acc	451
Val Asp Met Lys Ser Gly Leu Ala Val Tyr Leu His Thr Phe Ala Thr	
105 110 115	
ttg gcc acg tgg acc gag ctt aaa cat gat ttg acg ctg att gag tat	499
Leu Ala Thr Ser Thr Glu Leu Lys His Asp Leu Thr Leu Ile Ala Tyr	
120 125 130	
gaa ttc aac gaa gtt ggt gat aac ctt aat ggt ttg ggc aac att ctt	547
Glu Cys Glu Glu Val Ala Asp His Leu Asn Gly Leu Gly His Ile Arg	
135 140 145	
gat gag cat ctc aac tgg ttg ggg ggt gat ttg ggg ttg ctg ggt gag	595
Asp Glu His Pro Glu Trp Leu Ala Ala Asp Leu Ala Leu Leu Gly Glu	
150 155 160 165	
cct act ggc gcc tgg act gag ggg gcc tgc cag gcc aat ctt cgc atc	643
Pro Thr Gly Gly Trp Ile Glu Ala Gly Cys Glu Gly Asn Leu Arg Ile	
170 175 180	
aag gtg acg ggg cat ggt gtg ggt gcc cat tgg ggg aga aac tgg ttg	691
Lys Val Thr Ala His Gly Val Arg Ala His Ser Ala Arg Ser Trp Leu	
185 190 195	
ggt gat aat ggg atg cat aag ttg tgg cgg atc att tgg aag gtt gat	739
Gly Asp Asn Ala Met His Lys Leu Ser Pro Ile Ile Ser Lys Val Ala	
200 205 210	
ggg tat aag gcc gca gaa gtc aac att gat ggc ttg acc tac cgt gaa	787
Ala Tyr Lys Ala Ala Glu Val Asn Ile Asp Gly Leu Thr Tyr Arg Glu	
215 220 225	
ggc ctc aac atc gtt ttc tgc gaa tgg ggc gtg gca aac aac gtc att	835
Gly Leu Asn Ile Val Phe Cys Glu Ser Gly Val Ala Asn Asn Val Ile	
230 235 240 245	
cca gac ctc ggg tgg atg aac ctc aac ttc cgt ttc ggg cgg aat cgc	883
Pro Asp Leu Ala Trp Met Asn Leu Asn Phe Arg Phe Ala Pro Asn Arg	
250 255 260	
gat ctc aac gag ggg atc gag cat gtc gtc gaa acg ctt gag ctt gac	931
Asp Leu Asn Glu Ala Ile Glu His Val Val Glu Thr Leu Glu Leu Asp	
265 270 275	
ggt caa gac gcc atc gaa tgg gcc gta gaa gac ggg gca gcc ggt gcc	979
Gly Gln Asp Gly Ile Glu Trp Ala Val Glu Asp Gly Ala Gly Gly Ala	
280 285 290	
ctt cca gcc ttg ggg cag cag gtg aca agc ggg ctt atc gac gcc gtc	1027

Leu Pro Gly Leu Gly Gln Gln Val Thr Ser Gly Leu Ile Asp Ala Val
 295 300 305
 ggc cgc gaa aaa atc cgc gca aaa ttc ggc tgg acc gat gtc tca cgt 1075
 Gly Arg Glu Lys Ile Arg Ala Lys Phe Gly Trp Thr Asp Val Ser Arg
 310 315 320 325
 ttc tca gcc atg gga att cca gcc cta aac ttt ggc tct ggt gat cca 1123
 Phe Ser Ala Met Gly Ile Pro Ala Leu Asn Phe Gly Ala Gly Asp Pro
 330 335 340
 agt ttc ggc cat aaa cgc gac gag cag tgc cca gtc gag caa atc acg 1171
 Ser Phe Ala His Lys Arg Asp Glu Gln Cys Pro Val Glu Gln Ile Thr
 345 350 355
 gat gtc gca gca att ttg aag cag ttc ctg agc gag taacgatt 1217
 Asp Val Ala Ala Ile Leu Lys Gln Tyr Leu Ser Glu
 360 365
 cgggggttacc atg 1230

<210> 30
 <211> 360
 <212> CRT
 <213> Corynebacterium glutamicum

<100> 30
 Val Asn Ser Glu Leu Lys Pro Gly Leu Asp Leu Leu Gly Asp Pro Ile
 1 5 10 15
 Val Leu Thr Gln Arg Leu Val Asp Ile Pro Ser Pro Ser Gly Gln Glu
 20 25 30
 Lys Glu Ile Ala Asp Glu Ile Glu Asp Ala Leu Arg Asn Leu Asn Leu
 35 40 45
 Pro Gly Val Glu Val Phe Arg Phe Asn Asn Asn Val Leu Ala Arg Thr
 50 55 60
 Asn Arg Gly Leu Ala Ser Arg Val Met Leu Ala Gly His Ile Asp Thr
 65 70 75 80
 Val Pro Ile Ala Asp Asn Leu Pro Ser Arg Val Glu Asp Gly Ile Met
 85 90 95
 Tyr Gly Cys Gly Thr Val Asp Met Lys Ser Gly Leu Ala Val Tyr Leu
 100 105 110
 His Thr Phe Ala Thr Leu Ala Thr Ser Thr Glu Leu Lys His Asp Leu
 115 120 125
 Thr Leu Ile Ala Tyr Glu Cys Glu Glu Val Ala Asp His Leu Asn Gly
 130 135 140
 Leu Gly His Ile Arg Asp Glu His Pro Glu Trp Leu Ala Ala Asp Leu
 145 150 155 160
 Ala Leu Leu Gly Glu Pro Thr Gly Gly Trp Ile Glu Ala Gly Cys Gln
 165 170 175

Gly Asn Leu Arg Ile Lys Val Thr Ala His Gly Val Arg Ala His Ser
180 185 190

Ala Arg Ser Trp Leu Gly Asp Asn Ala Met His Lys Leu Ser Pro Ile
195 200 205

Ile Ser Lys Val Ala Ala Tyr Lys Ala Ala Glu Val Asn Ile Asp Gly
210 215 220

Leu Thr Tyr Arg Glu Gly Leu Asn Ile Val Phe Cys Glu Ser Gly Val
225 230 235 240

Ala Asn Asn Val Ile Pro Asp Leu Ala Trp Met Asn Leu Asn Phe Arg
245 250 255

Ile Ala Pro Asn Arg Asp Leu Asn Glu Ala Ile Glu His Val Val Glu
260 265 270

Thr Leu Glu Leu Asp Gly Gln Asp Gly Ile Glu Trp Ala Val Glu Asp
275 280 285

Gly Ala Gly Gly Ala Leu Pro Gly Leu Gly Gln Gln Val Thr Ser Gly
290 295 300

Leu Ile Asp Ala Val Gly Arg Glu Lys Ile Arg Ala Lys Phe Gly Trp
305 310 315 320

Thr Asp Val Ser Arg Phe Ser Ala Met Gly Ile Pro Ala Leu Asn Phe
325 330 335

Gly Ala Gly Asp Pro Ser Phe Ala His Lys Arg Asp Glu Gln Cys Pro
340 345 350

Val Glu Gln Ile Thr Asp Val Ala Ala Ile Leu Lys Gln Tyr Leu Ser
355 360 365

Glu

<210> 11

<211> 1069

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1036)

<223> EXA00044

<400> 31

attactctag ccttccaage tgatgatgca ttacttaaaa actgcagaca cttgaaaaaac 60

ttctcaaccg cactcgttcc ctcaaccac aaggagcacc atg gct tcc gca act 115
Met Ala Ser Ala Thr
1 5

ttc acc ggc gtg atc cca ccc gta atg acc cca ctc cag gcc gac gcc 163
Phe Thr Gly Val Ile Pro Pro Val Met Thr Pro Leu His Ala Asp Gly
10 15 20

agt gtg gat gta gaa agc ctc cgc aag ctc gtt gac cac ctc atc aat	211
Ser Val Asp Val Glu Ser Leu Arg Lys Leu Val Asp His Leu Ile Asn	
25 30 35	
ggg ggc gtc gac gga ctt ttc gca ctg ggc tcc tca ggc gaa ggc gca	259
Gly Gly Val Asp Gly Leu Phe Ala Leu Gly Ser Ser Gly Glu Ala Ala	
40 45 50	
ttc ctc acc cgc gcc cag cgc aaa ctc gca ctg acc acc atc atc gag	307
Phe Leu Thr Arg Ala Gln Arg Lys Leu Ala Leu Thr Thr Ile Ile Glu	
55 60 65	
cac acc gca ggc cgc ggt ccc gca act gct ggt gtc att gaa acc acc	355
His Thr Ala Gly Arg Val Pro Val Thr Ala Gly Val Ile Glu Thr Thr	
70 75 80 85	
act gat cgc gtg att gag ctc ggc gaa gat gcc ctg gag gtt ggt gcc	403
Thr Ala Arg Val Ile Glu Leu Val Glu Asp Ala Leu Glu Ala Gly Ala	
90 95 100	
gaa ggc ttc gtt gcc act gca cct ttc tac acc cgc acc cac gat gtg	451
Glu Gly Leu Val Ala Thr Ala Pro Phe Tyr Thr Arg Thr His Asp Val	
105 110 115	
gaa att gaa gaa cac ttc cgc aag atc cac gcc gcc gct cca gag ctt	499
Glu Ile Glu Glu His Phe Arg Lys Ile His Ala Ala Ala Pro Glu Leu	
120 125 130	
cca ctg ttc gcc tac aac atc cca ggc tcc ggc cac tcc acc ttc acc	547
Pro Leu Phe Ala Tyr Asn Ile Pro Val Ser Val His Ser Asn Leu Asn	
135 140 145	
cca gtc atc ctt ttg acc ctg gcc aag gat gcc gtt ctt gaa tgc acc	595
Pro Val Met Leu Leu Thr Leu Ala Lys Asp Gly Val Leu Ala Gly Thr	
150 155 160 165	
aag gat tcc agt gcc aat gat gcc gca atc cgc tca ctg acc gaa gct	643
Lys Asp Ser Ser Gly Asn Asp Gly Ala Ile Arg Ser Leu Ile Glu Ala	
170 175 180	
cgt gat gat gat gga ctc act gag cag ttc aag atc ctc acc gcc agc	691
Arg Asp Asp Ala Gly Leu Thr Glu Gln Phe Lys Ile Leu Thr Gly Ser	
185 190 195	
gaa acc acc gtt gat ttc gcc tac ctt gcg ggt gcc gat gga gtt gtc	739
Glu Thr Thr Val Asp Phe Ala Tyr Leu Ala Gly Ala Asp Gly Val Val	
200 205 210	
cca gcc ctg gcc aat gtt gat cct gca gca tac gca gct tta gca aaa	787
Pro Gly Leu Gly Asn Val Asp Pro Ala Ala Tyr Ala Ala Leu Ala Lys	
215 220 225	
ctc tgc ctc gat gga aag tgg gca gaa gct gct gct ttg cag aag cgc	835
Leu Cys Leu Asp Gly Lys Trp Ala Glu Ala Ala Leu Gln Lys Arg	
230 235 240 245	
atc aac cac ctc ttc cac atc gtc ttc gtg gga gac acc tcc cat atg	883
Ile Asn His Leu Phe His Ile Val Phe Val Gly Asp Thr Ser His Met	
250 255 260	
tcc gga tcc age gct ggt ttg gcc ggt ttc aag aca gca ctc gca cac	931

Ser Gly Ser Ser Ala Gly Leu Gly Gly Phe Lys Thr Ala Leu Ala His
265 270 275

ctt ggc att att gaa tcc aat ggc atg gca gtt cct cac cag agc etc 979
Leu Gly Ile Ile Glu Ser Asn Ala Met Ala Val Pro His Gln Ser Leu
280 285 290

agc gac gaa gaa act gct ggc att cac ggc att gtt gat gaa ttc atg 1027
Ser Asp Glu Glu Thr Ala Arg Ile His Ala Ile Val Asp Glu Phe Leu
295 300 305

tac acc gct taaggccac acccactgac tga 1059
Tyr thr Ala
310

<210> 32

<211> 312

<212> PRT

<213> Corynebacterium glutamicum

<400> 32

Met Ala Ser Ala Thr Phe Thr Gly Val Ile Pro Pro Val Met Thr Pro
1 5 10 15

Leu His Ala Asp Gly Ser Val Asp Val Glu Ser Leu Arg Lys Leu Val
20 25 30

Asp His Leu Ile Asn Gly Gly Val Asp Gly Leu Phe Ala Leu Gly Ser
35 40 45

Ser Gly Glu Ala Ala Phe Leu Thr Arg Ala Gln Arg Lys Leu Ala Leu
50 55 60

Thr Thr Ile Ile Glu His Thr Ala Gly Arg Val Pro Val Thr Ala Gly
65 70 75 80

Val Ile Glu Thr Thr Thr Ala Arg Val Ile Glu Leu Val Glu Asp Ala
85 90 95

Leu Glu Ala Gly Ala Glu Gly Leu Val Ala Thr Ala Pro Phe Tyr Thr
100 105 110

Arg Thr His Asp Val Glu Ile Glu Glu His Phe Arg Lys Ile His Ala
115 120 125

Ala Ala Pro Glu Leu Pro Leu Phe Ala Tyr Asn Ile Pro Val Ser Val
130 135 140

His Ser Asn Leu Asn Pro Val Met Leu Leu Thr Leu Ala Lys Asp Gly
145 150 155 160

Val Leu Ala Gly Thr Lys Asp Ser Ser Gly Asn Asp Gly Ala Ile Arg
165 170 175

Ser Leu Ile Glu Ala Arg Asp Asp Ala Gly Leu Thr Glu Gln Phe Lys
180 185 190

Ile Leu Thr Gly Ser Glu Thr Thr Val Asp Phe Ala Tyr Leu Ala Gly
195 200 205

Ala Asp Gly Val Val Pro Gly Leu Gly Asn Val Asp Pro Ala Ala Tyr
 210 215 220

Ala Ala Leu Ala Lys Leu Cys Leu Asp Gly Lys Trp Ala Glu Ala Ala
 225 230 235 240

Ala Leu Gln Lys Arg Ile Asn His Leu Phe His Ile Val Phe Val Gly
 245 250 255

Asp Thr Ser His Met Ser Gly Ser Ser Ala Gly Leu Gly Gly Phe Lys
 260 265 270

Thr Ala Leu Ala His Leu Gly Ile Ile Glu Ser Asn Ala Met Ala Val
 275 280 285

Pro His Gln Ser Leu Ser Asp Glu Glu Thr Ala Arg Ile His Ala Ile
 290 295 300

Val Asp Glu Phe Leu Tyr Thr Ala
 305 310

<210> 33
 <211> 867
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)...(844)
 <223> RXA00823

<400> 33
 aacgggtcagt taggtatgga tatcagcacc ttctgaacgg gtacgtctag actgggtgggc 60

gtttgaaaaa ctcttcggcc caagaaaatg aaggagcata atg gga atc aag gtt 115
 Met Gly Ile Lys Val
 1 5

ggc gtt ctg gga gcc aaa ggc cgt gtt ggt caa act att gtg gca gca 163
 Gly Val Leu Gly Ala Lys Gly Arg Val Gly Gln Thr Ile Val Ala Ala
 10 15 20

gtc aat gag tcc gac gat ctg gag ctt gtt gca gag atc ggc gtc gac 211
 Val Asn Glu Ser Asp Asp Leu Glu Leu Val Ala Glu Ile Gly Val Asp
 25 30 35

gat gat ttg agc ctt ctg gta gac aac ggc gct gaa gtt gtc gtt gac 259
 Asp Asp Leu Ser Leu Leu Val Asp Asn Gly Ala Glu Val Val Val Asp
 40 45 50

ttc acc act cct aac gct gtg atg ggc aac ctg gag ttc tgc atc aac 307
 Phe Thr Thr Pro Asn Ala Val Met Gly Asn Leu Glu Phe Cys Ile Asn
 55 60 65

aac ggc att tct ggc gtt gtt gga acc acg ggc ttc gat gat gct cgt 355
 Asn Gly Ile Ser Ala Val Val Gly Thr Thr Gly Phe Asp Asp Ala Arg
 70 75 80 85

ttg gag cag gtt cgc gac tgg ctt gaa gga aaa gac aat gtc ggt gtt 403
 Leu Glu Gln Val Arg Asp Trp Leu Glu Gly Lys Asp Asn Val Gly Val

190

ATA GGC CTG TAAAGGCTCA TTTCAGCAGC GGG 867
Leu Gly Leu

```

:210> 34
:211> 248
:212> PRT
:213> Corynebacterium glutamicum

```

```

1400> 34
Met Gly Ile Lys Val Gly Val Leu Gly Ala Lys Gly Arg Val Gly Gln
  1             5             10             15

Thr Ile Val Ala Ala Val Asn Glu Ser Asp Asp Leu Glu Leu Val Ala
      20             25             30

Glu Ile Gly Val Asp Asp Asp Leu Ser Leu Leu Val Asp Asn Gly Ala
  35             40             45

Glu Val Val Val Asp Phe Thr Thr Pro Asn Ala Val Met Gly Asn Leu
  50             55             60

```

Glu Phe Cys Ile Asn Asn Gly Ile Ser Ala Val Val Gly Thr Thr Gly
 65 70 75 80
 Phe Asp Asp Ala Arg Leu Glu Gln Val Arg Asp Trp Leu Glu Gly Lys
 85 90 95
 Asp Asn Val Gly Val Leu Ile Ala Pro Asn Phe Ala Ile Ser Ala Val
 100 105 110
 Leu Thr Met Val Phe Ser Lys Gln Ala Ala Arg Phe Phe Glu Ser Ala
 115 120 125
 Glu Val Ile Glu Leu His His Pro Asn Lys Leu Asp Ala Pro Ser Gly
 130 135 140
 Thr Ala Ile His Thr Ala Gln Gly Ile Ala Ala Ala Arg Lys Glu Ala
 145 150 155 160
 Gly Met Asp Ala Gln Pro Asp Ala Thr Glu Gln Ala Leu Glu Gly Ser
 165 170 175
 Arg Gly Ala Ser Val Asp Gly Ile Pro Val His Ala Val Arg Met Ser
 180 185 190
 Gly Met Val Ala His Glu Gln Val Ile Phe Gly Thr Gln Gly Gln Thr
 195 200 205
 Leu Thr Ile Lys Gln Asp Ser Tyr Asp Arg Asn Ser Phe Ala Pro Gly
 210 215 220
 Val Leu Val Gly Val Arg Asn Ile Ala Gln His Pro Gly Leu Val Val
 225 230 235 240
 Gly Leu Glu His Tyr Leu Gly Leu
 245

<210> 35
 <211> 873
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(850)
 <223> EXA00864

<400> 35
 acagcaccda ggctagtcg taggaattga gcattacctt ggctgtaaa ggcctatttc 60
 agcagcgggt ggaatttttt aaaaggagcg tttaaagggt gtg gcc gaa caa gtt 115
 Val Ala Glu Gln Val
 1 5
 aaa ttg agc gtg gag ttg ata gcg tgc agt tct ttt act cca ccc gct 163
 Lys Leu Ser Val Glu Leu Ile Ala Cys Ser Ser Phe Thr Pro Pro Ala
 10 15 20
 gat gtt gag tgg tca act gat gtt gag gcc gcc gaa gca ctc gtc gag 211
 Asp Val Glu Trp Ser Thr Asp Val Glu Gly Ala Glu Ala Leu Val Glu
 25 30 35

ttt ggg ggt cgt gcc tgc tac gaa act ttt gat aag cgg aac cct cga 259
 Phe Ala Gly Arg Ala Cys Tyr Glu Thr Phe Asp Lys Pro Asn Pro Arg
 40 45 50

act gct tcc aat gct ggg tat ctg cgc cac atc atg gaa gtg ggg cac 307
 Thr Ala Ser Asn Ala Ala Tyr Leu Arg His Ile Met Glu Val Gly His
 55 60 65

act gct ttg ctt gag cat gcc aat gcc acg atg tat atc cga ggc att 355
 Thr Ala Leu Leu Glu His Ala Asn Ala Thr Met Tyr Ile Arg Gly Ile
 70 75 80 85

tat cgg tcc ggg acc cat gaa ttg gtc cga cac cgc cat ttt tcc ttc 403
 Ser Arg Ser Ala Thr His Glu Leu Val Arg His Arg His Phe Ser Phe
 90 95 100

tat caa ctg tct cag cgt ttc gtc cac agc gga gaa tgg gaa gta gtg 451
 Ser Gln Leu Ser Gln Arg Phe Val His Ser Gly Glu Ser Glu Val Val
 105 110 115

gtg ccc att ctg atc gat gaa gat cgg cag ttg cgt gaa cat ttc atg 499
 Val Pro Thr Leu Ile Asp Gln Asp Pro Gln Leu Arg Glu Leu Phe Met
 120 125 130

cac gcc atg gat gaa tat cgg ttc gct ttc aat gac ctg ctt aat gag 547
 His Ala Met Asp Glu Ser Arg Phe Ala Phe Asn Glu Leu Leu Asn Ala
 135 140 145

ctg gaa gaa aaa ctt ggc gat gaa cgg aat gca ctt tta agg aaa aag 595
 Leu Glu Glu Lys Leu Gly Asp Glu Pro Asn Ala Leu Leu Arg Lys Lys
 150 155 160 165

cag gct cgt caa gca gct cga gct gtg ctg ccc aac gtt aca gag tcc 643
 Gln Ala Arg Gln Ala Ala Arg Ala Val Leu Pro Asn Ala Thr Glu Ser
 170 175 180

aga atc gtg gtg tct gga aac ttc cgc acc tgg agg cat ttc att ggc 691
 Arg Ile Val Val Ser Gly Asn Phe Arg Thr Trp Arg His Phe Ile Gly
 185 190 195

atg cga gcc agt gaa cat gca gac gtc gaa atc cgc gaa gta ggg gta 739
 Met Arg Ala Ser Glu His Ala Asp Val Glu Ile Arg Glu Val Ala Val
 200 205 210

gaa tgt tta aga aag ctg cag gta gca gcg cca act gtt ttc ggt gat 787
 Glu Cys Leu Arg Lys Leu Gln Val Ala Ala Pro Thr Val Phe Gly Asp
 215 220 225

ttt gag att gaa act ttg gca gac gga tgg caa atg gca aca agc cgg 835
 Phe Glu Ile Glu Thr Leu Ala Asp Gly Ser Gln Met Ala Thr Ser Pro
 230 235 240 245

tat gtc atg gac ttt taacgcaaaag ctcacaccca cga 873
 Tyr Val Met Asp Phe
 250

<210> 36
 <211> 250
 <212> PRT

<213> Corynebacterium glutamicum

<400> 36

```

Val Ala Glu Gln Val Lys Leu Ser Val Glu Leu Ile Ala Cys Ser Ser
 1           5           10           15

Phe Thr Pro Pro Ala Asp Val Glu Trp Ser Thr Asp Val Glu Gly Ala
 20           25           30

Glu Ala Leu Val Glu Phe Ala Gly Arg Ala Cys Tyr Glu Thr Phe Asp
 35           40           45

Lys Pro Asn Pro Arg Thr Ala Ser Asn Ala Ala Tyr Leu Arg His Ile
 50           55           60

Met Glu Val Gly His Thr Ala Leu Leu Glu His Ala Asn Ala Thr Met
 65           70           75           80

Tyr Ile Arg Gly Ile Ser Arg Ser Ala Thr His Glu Leu Val Arg His
 85           90           95

Arg His Phe Ser Phe Ser Gln Leu Ser Gln Arg Phe Val His Ser Gly
100           105           110

Glu Ser Glu Val Val Val Pro Thr Leu Ile Asp Glu Asp Pro Gln Leu
115           120           125

Arg Glu Leu Phe Met His Ala Met Asp Glu Ser Arg Phe Ala Phe Asn
130           135           140

Glu Leu Leu Asn Ala Leu Glu Glu Lys Leu Gly Asp Glu Pro Asn Ala
145           150           155           160

Leu Leu Arg Lys Lys Gln Ala Arg Gln Ala Ala Arg Ala Val Leu Pro
165           170           175

Asn Ala Thr Glu Ser Arg Ile Val Val Ser Gly Asn Phe Arg Thr Trp
180           185           190

Arg His Phe Ile Gly Met Arg Ala Ser Glu His Ala Asp Val Glu Ile
195           200           205

Arg Glu Val Ala Val Glu Cys Leu Arg Lys Leu Gln Val Ala Ala Pro
210           215           220

Thr Val Phe Gly Asp Phe Glu Ile Glu Thr Leu Ala Asp Gly Ser Gln
225           230           235           240

Met Ala Thr Ser Pro Tyr Val Met Asp Phe
245           250

```

<210> 37

<211> 608

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (69)..(608)

<223> RXA02843

<400> 37

cccattgogc ggaggtogca ccccttcoga cttgaactga taggcogata gaaattattc 60

tggacgtc atg act act gct tcc gca acc gga att gca aca ctg acc tcc 110

Met Thr Thr Ala Ser Ala Thr Gly Ile Ala Thr Leu Thr Ser

1

5

10

acc ggc gac ttc ctg gac gtg tgg tat cca gaa atc ggg tcc acc gac 158

Thr Gly Asp Val Leu Asp Val Trp Tyr Pro Glu Ile Gly Ser Thr Asp

15

20

25

30

cag tcc ggc ctg aca cct cta gaa ggc gtc gat gaa gat cga aac gtc 206

Gln Ser Ala Leu Thr Pro Leu Glu Gly Val Asp Glu Asp Arg Asn Val

35

40

45

acc cgc aaa atc gtg acc aca act atc gac acc gac gca gcc ccc acc 254

Thr Arg Lys Ile Val Thr Thr Thr Ile Asp Thr Asp Ala Ala Pro Thr

50

55

60

gac acc tac gat gca tgg ctg cgc ctt cac ctg ctg tcc cag cgc gtt 302

Asp Thr Tyr Asp Ala Trp Leu Arg Leu His Leu Leu Ser His Arg Val

65

70

75

ttc cgc ctt cag acc atc aac cta gac ggc att ttc ggc ttc ctg aac 350

Phe Arg Pro His Thr Ile Asn Leu Asp Gly Ile Phe Gly Leu Leu Asn

80

85

90

aat gtc gtc tgg acc aac ttc gga ctt tgc gaa att gat agt ttc gaa 398

Asn Val Val Trp Thr Asn Phe Gly Pro Cys Ala Val Asp Gly Phe Ala

95

100

105

110

ctc acc cgc ggc cgc ctg tca cgc cga ggc caa gtt acc gtt tat agc 446

Leu Thr Arg Ala Arg Leu Ser Arg Arg Gly Gln Val Thr Val Tyr Ser

115

120

125

gtc gac aag ttc cca cgc atg gtc gac tat gtg gtt ccc tgc ggc gtg 494

Val Asp Lys Phe Pro Arg Met Val Asp Tyr Val Val Pro Ser Gly Val

130

135

140

cgc atc ggt gac gcc gac cgc gtc cga ctt ggc gcg tac ctg gca gat 542

Arg Ile Gly Asp Ala Asp Arg Val Arg Leu Gly Ala Tyr Leu Ala Asp

145

150

155

ggc acc acc gtg atg cat gag ggc ttc gtg aac ttc aac gct ggc acc 590

Gly Thr Thr Val Met His Glu Gly Phe Val Asn Phe Asn Ala Gly Thr

160

165

170

ctc ggc gct tcc atg gtt 608

Leu Gly Ala Ser Met Val

175

180

<210> 38

<211> 180

<212> PRT

<213> Corynebacterium glutamicum

<400> 38

Met Thr Thr Ala Ser Ala Thr Gly Ile Ala Thr Leu Thr Ser Thr Gly

1

5

10

15

Asp Val Leu Asp Val Trp Tyr Pro Glu Ile Gly Ser Thr Asp Gln Ser
 20 25 30
 Ala Leu Thr Pro Leu Glu Gly Val Asp Glu Asp Arg Asn Val Thr Arg
 35 40 45
 Lys Ile Val Thr Thr Thr Ile Asp Thr Asp Ala Ala Pro Thr Asp Thr
 50 55 60
 Tyr Asp Ala Trp Leu Arg Leu His Leu Leu Ser His Arg Val Phe Arg
 65 70 75 80
 Pro His Thr Ile Asn Leu Asp Gly Ile Phe Gly Leu Leu Asn Asn Val
 85 90 95
 Val Trp Thr Asn Phe Gly Pro Cys Ala Val Asp Gly Phe Ala Leu Thr
 100 105 110
 Arg Ala Arg Leu Ser Arg Arg Gly Gln Val Thr Val Tyr Ser Val Asp
 115 120 125
 Lys Phe Pro Arg Met Val Asp Tyr Val Val Pro Ser Gly Val Arg Ile
 130 135 140
 Gly Asp Ala Asp Arg Val Arg Leu Gly Ala Tyr Leu Ala Asp Gly Thr
 145 150 155 160
 Thr Val Met His Glu Gly Phe Val Asn Phe Asn Ala Gly Thr Leu Gly
 165 170 175
 Ala Ser Met Val
 180

<010> 39
 <011> 1143
 <012> DNA
 <013> Corynebacterium glutamicum

<020>
 <021> CDS
 <022> (101)..(1120)
 <023> EXN00355

<000> 39
 atagatcag cgcacccgtg gtggaaccaa aaggctcaac aatacgaac gttcgtttc 60
 gctcctgatg aaagagatgt cccatgaatca tcactaagt atg cat ctc ggt aag 115
 Met His Leu Gly Lys
 1 5
 ctc gag cag gac agt gcc acc aca att ttg gag gat tac aag aac atg 163
 Leu Asp Gln Asp Ser Ala Thr Thr Ile Leu Glu Asp Tyr Lys Asn Met
 10 15 20
 acc aac atc cgc gta gct atc gtg ggc tac gga aac ctg gga cgc agc 211
 Thr Asn Ile Arg Val Ala Ile Val Gly Tyr Gly Asn Leu Gly Arg Ser
 25 30 35
 gtc gaa aag ctt att gcc aag cag ccc gac atg gac ctt gta gga atc 259

Val	Glu	Lys	Leu	Ile	Ala	Lys	Gln	Pro	Asp	Met	Asp	Leu	Val	Gly	Ile		
		40					45					50					
ttc	tcc	cgc	ggg	gcc	acc	ctc	gac	aca	aag	acg	cca	gtc	ttt	gat	gtc	307	
Phe	Ser	Arg	Arg	Ala	Thr	Leu	Asp	Thr	Lys	Thr	Pro	Val	Phe	Asp	Val		
	55					60					65						
gcc	gac	gtg	gac	aag	cac	gcc	gac	gac	gtg	gac	gtg	ctg	ttc	ctg	tgc	355	
Ala	Asp	Val	Asp	Lys	His	Ala	Asp	Asp	Val	Asp	Val	Leu	Phe	Leu	Cys		
	70				75					80					85		
atg	gac	tcg	gcc	acc	gac	atc	cct	gag	cag	gca	cca	aag	ttc	gag	cag	403	
Met	Gly	Ser	Ala	Thr	Asp	Ile	Pro	Glu	Gln	Ala	Pro	Lys	Phe	Ala	Gln		
				90				95						100			
ttc	gcc	tgc	acc	gta	gac	acc	tac	gac	aac	cac	cgc	gac	atc	cca	cgc	451	
Phe	Ala	Cys	Thr	Val	Asp	Thr	Tyr	Asp	Asn	His	Arg	Asp	Ile	Pro	Arg		
			105					110					115				
cac	cgc	cag	gtc	atg	aac	gaa	gcc	gcc	acc	gca	gcc	ggc	aac	gtt	gca	499	
His	Arg	Gln	Val	Met	Asn	Glu	Ala	Ala	Thr	Ala	Ala	Gly	Asn	Val	Ala		
			120				125					130					
ctg	gac	tct	acc	ggc	tgg	cac	cca	gga	atg	ttc	tcg	atc	aac	cgc	gtc	547	
Leu	Val	Ser	Thr	Gly	Trp	Asp	Pro	Gly	Met	Phe	Ser	Ile	Asn	Arg	Val		
	135					140						145					
tac	tta	tta	tta	gtc	tta	ggt	gag	cac	cag	cag	cac	aac	ttc	tta	ggt	595	
Tyr	Ala	Ala	Ala	Val	Leu	Ala	Glu	His	Gln	Gln	His	Thr	Phe	Trp	Gly		
	150				155					160					165		
cca	ggt	ttg	tca	cag	ggc	cac	tcg	gat	gct	ttg	cga	cgc	atc	cct	ggc	643	
Pro	Gly	Leu	Ser	Gln	Gly	His	Ser	Asp	Ala	Leu	Arg	Arg	Ile	Pro	Gly		
				170					175					180			
gtt	caa	aac	cca	gtc	cac	tac	acc	ctc	cca	tcg	gaa	cac	ccc	ctg	gaa	691	
Val	Gln	Lys	Ala	Val	Gln	Tyr	Thr	Leu	Pro	Ser	Glu	Asp	Ala	Leu	Glu		
			185					190					195				
aag	gcc	cgc	cgc	ggc	gaa	gcc	ggc	gac	ctt	acc	gga	aag	caa	acc	cac	739	
Lys	Ala	Arg	Arg	Gly	Glu	Ala	Gly	Asp	Leu	Thr	Gly	Lys	Gln	Thr	His		
		200					205						210				
aag	cgc	caa	tgc	ttc	gtg	gtt	gcc	gac	ggg	gcc	gat	cac	gag	cgc	atc	787	
Lys	Arg	Gln	Cys	Phe	Val	Val	Ala	Asp	Ala	Ala	Asp	His	Glu	Arg	Ile		
	215					220					225						
gaa	aac	gac	atc	cgc	acc	atg	cct	gat	tac	ttc	gtt	ggc	tac	gaa	gtc	835	
Glu	Asn	Asp	Ile	Arg	Thr	Met	Pro	Asp	Tyr	Phe	Val	Gly	Tyr	Glu	Val		
	230					235					240				245		
gaa	gtc	aac	ttc	atc	gac	gaa	gca	acc	ttc	gac	tcg	gag	cac	acc	ggc	883	
Glu	Val	Asn	Phe	Ile	Asp	Glu	Ala	Thr	Phe	Asp	Ser	Glu	His	Thr	Gly		
			250						255					260			
atg	cca	cac	ggt	ggc	cac	gtg	att	acc	acc	ggc	gac	acc	ggt	ggc	ttc	931	
Met	Pro	His	Gly	Gly	His	Val	Ile	Thr	Thr	Gly	Asp	Thr	Gly	Gly	Phe		
			265					270						275			
aac	cac	acc	gtg	gaa	tac	atc	ctc	aag	ctg	gac	cga	aac	cca	gat	ttc	979	
Asn	His	Thr	Val	Glu	Tyr	Ile	Leu	Lys	Leu	Asp	Arg	Asn	Pro	Asp	Phe		

280 285 290

acc gct tcc tca cag atc gct ttc ggt cgc gca gct cac cgc atg aag 1027
 Thr Ala Ser Ser Gln Ile Ala Phe Gly Arg Ala Ala His Arg Met Lys
 295 300 305

cag cag ggc caa agc gga gct ttc acc atc ctc gaa gtt gct cca tac 1075
 Gln Gln Gly Gln Ser Gly Ala Phe Thr Val Leu Glu Val Ala Pro Tyr
 310 315 320 325

ctg ctc tcc cca gag aac ttg gac gat ctg atc gca cgc gac gtc 1120
 Leu Leu Ser Pro Glu Asn Leu Asp Asp Leu Ile Ala Arg Asp Val
 330 335 340

taatttagct cgaaggga gga 1143

<210> 40

<211> 340

<212> PRT

<213> Corynebacterium glutamicum

<400> 40

Met His Leu Gly Lys Leu Asp Gln Asp Ser Ala Thr Thr Ile Leu Glu
 1 5 10 15

Asp Tyr Lys Asn Met Thr Asn Ile Arg Val Ala Ile Val Gly Tyr Gly
 20 25 30

Asn Leu Gly Arg Ser Val Glu Lys Leu Ile Ala Lys Gln Pro Asp Met
 35 40 45

Asp Leu Val Gly Ile Phe Ser Arg Arg Ala Thr Leu Asp Thr Lys Thr
 50 55 60

Pro Val Phe Asp Val Ala Asp Val Asp Lys His Ala Asp Asp Val Asp
 65 70 75 80

Val Leu Phe Ile Cys Met Gly Ser Ala Thr Asp Ile Pro Glu Gln Ala
 85 90 95

Pro Lys Phe Ala Gln Phe Ala Cys Thr Val Asp Thr Tyr Asp Asn His
 100 105 110

Arg Asp Ile Pro Arg His Arg Gln Val Met Asn Glu Ala Ala Thr Ala
 115 120 125

Ala Gly Asn Val Ala Leu Val Ser Thr Gly Trp Asp Pro Gly Met Phe
 130 135 140

Ser Ile Asn Arg Val Tyr Ala Ala Ala Val Leu Ala Glu His Gln Gln
 145 150 155 160

His Thr Phe Trp Gly Pro Gly Leu Ser Gln Gly His Ser Asp Ala Leu
 165 170 175

Arg Arg Ile Pro Gly Val Gln Lys Ala Val Gln Tyr Thr Leu Pro Ser
 180 185 190

Glu Asp Ala Leu Glu Lys Ala Arg Arg Gly Glu Ala Gly Asp Leu Thr
 195 200 205

Gly Lys Gln Thr His Lys Arg Gln Cys Phe Val Val Ala Asp Ala Ala
 210 215 220

Asp His Glu Arg Ile Glu Asn Asp Ile Arg Thr Met Pro Asp Tyr Phe
 225 230 235 240

Val Gly Tyr Glu Val Glu Val Asn Phe Ile Asp Glu Ala Thr Phe Asp
 245 250 255

Ser Glu His Thr Gly Met Pro His Gly Gly His Val Ile Thr Thr Gly
 260 265 270

Asp Thr Gly Gly Phe Asn His Thr Val Glu Tyr Ile Leu Lys Leu Asp
 275 280 285

Arg Asn Pro Asp Phe Thr Ala Ser Ser Gln Ile Ala Phe Gly Arg Ala
 290 295 300

Ala His Arg Met Lys Gln Gln Gly Gln Ser Gly Ala Phe Thr Val Leu
 305 310 315 320

Glu Val Ala Pro Tyr Leu Leu Ser Pro Glu Asn Leu Asp Asp Leu Ile
 325 330 335

Ala Arg Asp Val
 340

<210> 41
 <211> 958
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(958)
 <223> FRXA00352

<400> 41
 aatagatcag cgcatacgtg gtggaaccaa aaggctcaac aatacgaaac gttagctttc 60

gttagctgag aaagagatgt cccgaatca tcatctaagt atg cat ctc ggt aag 115
 Met His Leu Gly Lys
 1 5

ctc gac cag gac agt gcc acc aca att ttg gag gat tac aag aac atg 163
 Leu Asp Gln Asp Ser Ala Thr Thr Ile Leu Glu Asp Tyr Lys Asn Met
 10 15 20

acc aac atc cgc gta gct atc gtg ggc tac gga aac ctg gga cgc agc 211
 Thr Asn Ile Arg Val Ala Ile Val Gly Tyr Gly Asn Leu Gly Arg Ser
 25 30 35

gtc gaa aag ctt att gcc aag cag ccc gac atg gac ctt gta gga atc 259
 Val Glu Lys Leu Ile Ala Lys Gln Pro Asp Met Asp Leu Val Gly Ile
 40 45 50

ttc tgg cgc cgg gcc acc ctc gac aca aag acg cca gtc ttt gat gtc 307
 Phe Ser Arg Arg Ala Thr Leu Asp Thr Lys Thr Pro Val Phe Asp Val
 55 60 65

gcc gac gtg gac aag cac gcc gac gac gtg gac gtg atg ttc atg tgc 355
 Ala Asp Val Asp Lys His Ala Asp Asp Val Asp Val Leu Phe Leu Cys
 70 75 80 85
 atg dgc tcc gcc acc gac atc cct gag cag gca cca aag ttc gag cag 403
 Met Gly Ser Ala Thr Asp Ile Pro Glu Gln Ala Pro Lys Phe Ala Gln
 90 95 100
 ttc gcc tgc acc gta gac acc tac gac aac caa cgc gac atc cca cgc 451
 Phe Ala Cys Thr Val Asp Thr Tyr Asp Asn His Arg Asp Ile Pro Arg
 105 110 115
 caa cgc cag atc atg aac gaa gcc gcc acc gca gcc gcc aac gtt gca 499
 His Arg Gln Val Met Asn Glu Ala Ala Thr Ala Ala Gly Asn Val Ala
 120 125 130
 atg gcc ttc acc gta tgc tat cca gga atg ttc tcc atc aac cgc gtc 547
 Leu Val Ser Thr Gly Trp Asp Pro Gly Met Phe Ser Ile Asn Arg Val
 135 140 145
 tac gaa gta gca gta tta tta gac cac cac cac tac aac ttc tta ggc 595
 Tyr Ala Ala Ala Val Leu Ala Glu His Gln Gln His Thr Phe Trp Gly
 150 155 160 165
 cca ggc ttc tca cag ggc cgc tcc gat att tta gta cgc atc cct ggc 643
 Pro Gly Leu Ser Gln Gly His Ser Asp Ala Leu Arg Arg Ile Pro Gly
 170 175 180
 gtt caa aag gca gtc cag tac acc ttc cca tcc gaa gac gcc atg gaa 691
 Val Gln Lys Ala Val Gln Tyr Thr Leu Pro Ser Glu Asp Ala Leu Glu
 185 190 195
 aag gcc cgc cgc gcc gaa gcc gcc gac ctt acc gga aag caa acc caa 739
 Lys Ala Arg Arg Gly Glu Ala Gly Asp Leu Thr Gly Lys Gln Thr His
 200 205 210
 aag cgc caa tgc ttc gtg gtt gcc gac gcg gcc gat caa gag cgc atc 787
 Lys Arg Gln Cys Phe Val Val Ala Asp Ala Ala Asp His Glu Arg Ile
 215 220 225
 gaa aac gac atc cgc acc atg cct gat tac ttc gtt ggc tac gaa gtc 835
 Glu Asn Asp Ile Arg Thr Met Pro Asp Tyr Phe Val Gly Tyr Glu Val
 230 235 240 245
 gaa gtc aac ttc atc gac gaa gca acc ttc gac tcc gag caa acc ggc 883
 Glu Val Asn Phe Ile Asp Glu Ala Thr Phe Asp Ser Glu His Thr Gly
 250 255 260
 atg cca caa ggt gcc caa gtg att acc acc gcc gac acc ggt gcc ttc 931
 Met Pro His Gly Gly His Val Ile Thr Thr Gly Asp Thr Gly Gly Phe
 265 270 275
 aac caa acc gtg gaa tac atc ttc aag 958
 Asn His Thr Val Glu Tyr Ile Leu Lys
 280 285

<210> 42
 <211> 286
 <212> PRT

<213> Corynebacterium glutamicum

<400> 42

```

Met His Leu Gly Lys Leu Asp Gln Asp Ser Ala Thr Thr Ile Leu Glu
  1          5          10          15

Asp Tyr Lys Asn Met Thr Asn Ile Arg Val Ala Ile Val Gly Tyr Gly
      20          25          30

Asn Leu Gly Arg Ser Val Glu Lys Leu Ile Ala Lys Gln Pro Asp Met
      35          40          45

Asp Leu Val Gly Ile Phe Ser Arg Arg Ala Thr Leu Asp Thr Lys Thr
      50          55          60

Pro Val Phe Asp Val Ala Asp Val Asp Lys His Ala Asp Asp Val Asp
      65          70          75          80

Val Leu Phe Leu Cys Met Gly Ser Ala Thr Asp Ile Pro Glu Gln Ala
      85          90          95

Pro Lys Phe Ala Gln Phe Ala Cys Thr Val Asp Thr Tyr Asp Asn His
     100          105          110

Arg Asp Ile Pro Arg His Arg Gln Val Met Asn Glu Ala Ala Thr Ala
     115          120          125

Ala Gly Asn Val Ala Leu Val Ser Thr Gly Trp Asp Pro Gly Met Phe
     130          135          140

Ser Ile Asn Arg Val Tyr Ala Ala Ala Val Leu Ala Glu His Gln Gln
     145          150          155          160

His Thr Phe Trp Gly Pro Gly Leu Ser Gln Gly His Ser Asp Ala Leu
     165          170          175

Arg Arg Ile Pro Gly Val Gln Lys Ala Val Gln Tyr Thr Leu Pro Ser
     180          185          190

Glu Asp Ala Leu Glu Lys Ala Arg Arg Gly Glu Ala Gly Asp Leu Thr
     195          200          205

Gly Lys Gln Thr His Lys Arg Gln Cys Phe Val Val Ala Asp Ala Ala
     210          215          220

Asp His Glu Arg Ile Glu Asn Asp Ile Arg Thr Met Pro Asp Tyr Phe
     225          230          235          240

Val Gly Tyr Glu Val Glu Val Asn Phe Ile Asp Glu Ala Thr Phe Asp
     245          250          255

Ser Glu His Thr Gly Met Pro His Gly Gly His Val Ile Thr Thr Gly
     260          265          270

Asp Thr Gly Gly Phe Asn His Thr Val Glu Tyr Ile Leu Lys
     275          280          285

```

<210> 43

<211> 1400

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(1377)

<223> RXA00972

<400> 43

cct	gca	cct	ggt	tgg	cgt	ttc	cgc	acc	gga	gaa	gat	gta	aca	atg	gct	48
Pro	Ala	Pro	Gly	Trp	Arg	Phe	Arg	Thr	Gly	Glu	Asp	Val	Thr	Met	Ala	
1			5						10					15		

aca	glt	gaa	aat	ttc	aat	gaa	ctt	ccc	gca	cac	gta	tgg	cca	cgc	aat	96
Thr	Val	Glu	Asn	Phe	Asn	Glu	Leu	Pro	Ala	His	Val	Trp	Pro	Arg	Asn	
		20						25					30			

gac	gtg	cgc	caa	gaa	gac	ggc	ggt	gtc	acc	gtc	gct	ggg	gtg	cct	ctg	144
Ala	Val	Arg	Gln	Glu	Asp	Gly	Val	Val	Thr	Val	Ala	Gly	Val	Pro	Leu	
		35					40					45				

ctt	gac	ctc	gct	gaa	gaa	tac	gga	acc	cca	cta	ttc	gta	gac	gag		192
Pro	Asp	Leu	Ala	Glu	Glu	Tyr	Gly	Thr	Pro	Leu	Phe	Val	Val	Asp	Glu	
	50					55					60					

gac	gat	ttc	cgt	tcc	cgc	tgt	cgt	gac	atg	gct	acc	gaa	ttc	ggg	gaa	240
Asp	Asp	Phe	Arg	Ser	Arg	Cys	Arg	Asp	Met	Ala	Thr	Ala	Phe	Gly	Gly	
	65				70				75					80		

caa	ggc	aat	gig	cac	tac	gaa	tct	aaa	gaa	ttc	ctg	acc	arg	atc	att	288
Pro	Gly	Asn	Val	His	Tyr	Ala	Ser	Lys	Ala	Phe	Leu	Thr	Lys	Thr	Ile	
				45				50						45		

gaa	cgt	tgg	glt	gat	gaa	gag	ggg	cta	gaa	ctg	gac	att	gaa	tcc	atc	336
Ala	Arg	Trp	Val	Asp	Glu	Glu	Gly	Leu	Ala	Leu	Asp	Ile	Ala	Ser	Ile	
		100					105					110				

aac	gaa	ctg	ggc	att	gac	ctg	gct	ggt	ttc	ccc	gac	agc	cgt	atc		384
Asn	Glu	Leu	Gly	Ile	Ala	Leu	Ala	Gly	Phe	Pro	Ala	Ser	Arg	Ile		
	115					120					125					

acc	gag	cac	ggc	aac	aac	aaa	ggc	gta	gag	ttc	ctg	cgc	ggg	ttg	ggt	432
Thr	Ala	His	Gly	Asn	Asn	Lys	Gly	Val	Glu	Phe	Leu	Arg	Ala	Leu	Val	
	130					135					140					

caa	aac	ggt	gtg	gga	cac	gtg	gtg	ctg	gac	tcc	gca	cag	gaa	cta	gaa	480
Gln	Asn	Gly	Val	Gly	His	Val	Val	Leu	Asp	Ser	Ala	Gln	Glu	Leu	Glu	
	145				150				155					160		

ctg	ttg	gat	tac	ggt	gac	gct	ggt	gaa	ggc	aag	att	cag	gac	gtg	ttg	528
Leu	Leu	Asp	Tyr	Val	Ala	Ala	Gly	Glu	Gly	Lys	Ile	Gln	Asp	Val	Leu	
		165					170						175			

atc	cgc	gta	aag	cca	ggc	atc	gaa	gca	cac	acc	cac	gag	ttc	atc	gac	576
Ile	Arg	Val	Lys	Pro	Gly	Ile	Glu	Ala	His	Thr	His	Glu	Phe	Ile	Ala	
		180					185					190				

act	agc	cac	gaa	gac	cag	aag	tcc	gga	ttc	tcc	ctg	gca	tcc	ggt	tcc	624
Thr	Ser	His	Glu	Asp	Gln	Lys	Phe	Gly	Phe	Ser	Leu	Ala	Ser	Gly	Ser	
	195					200					205					

gaa	ttc	gaa	gaa	gca	aaa	ggc	gct	aac	aac	gaa	gaa	aac	ctg	aac	ctg	672
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

Ala Phe Glu Ala Ala Lys Ala Ala Asn Asn Ala Glu Asn Leu Asn Leu	
210 215 220	
gtt ggc ctg cac tgc cac gtt ggt tcc cag gtg ttc gac gcc gaa ggc	720
Val Gly Leu His Cys His Val Gly Ser Gln Val Phe Asp Ala Glu Gly	
225 230 235 240	
ttc aag ctg gaa gaa gaa cgc gtg ttg ggc ctg tac tca cag atc cac	768
Phe Lys Leu Ala Ala Glu Arg Val Leu Gly Leu Tyr Ser Gln Ile His	
245 250 255	
agc gaa ctg ggc gtt gcc ctt cct gaa ctg gat ctc ggt ggc gga tac	816
Ser Glu Leu Gly Val Ala Leu Pro Glu Leu Asp Leu Gly Gly Gly Tyr	
260 265 270	
ggc att gcc tat acc gaa gct gaa gaa cca ctc aac gtc gaa gaa gtt	864
Gly Ile Ala Tyr Thr Ala Ala Glu Glu Pro Leu Asn Val Ala Glu Val	
275 280 285	
gcr ccr gac ctg ttc acc gaa gtc gaa aaa atg gaa gtc gaa cta gcc	912
Ala Ser Asp Leu Leu Thr Ala Val Gly Lys Met Ala Ala Glu Leu Gly	
290 295 300	
atc gac gaa cca acc gtg ctt gtt gag ccc ggc cgc gct atc gaa ggc	960
Ile Asp Ala Pro Thr Val Leu Val Glu Pro Gly Arg Ala Ile Ala Gly	
305 310 315 320	
ccc tcc aac gtg acc atc tac gaa gtc ggc aac aac aaa gac gtc ccc	1008
Pro Ser Thr Val Thr Ile Tyr Glu Val Gly Thr Thr Lys Asp Val His	
325 330 335	
ata gac gac gac aaa acc cgc cgt tac atc ccc gtg gac gaa ggc atg	1056
Val Asp Asp Asp Lys Thr Arg Arg Tyr Ile Ala Val Asp Gly Gly Met	
340 345 350	
tcc gac aac atc cgc cca gaa ctc tac ggg tcc gaa tac gac gcc cgc	1104
Ser Asp Asn Ile Arg Pro Ala Leu Tyr Gly Ser Glu Tyr Asp Ala Arg	
355 360 365	
gta gta tcc cgc ttc gcc gaa gaa gac cca gta agc acc cgc atc gtg	1152
Val Val Ser Arg Phe Ala Glu Gly Asp Pro Val Ser Thr Arg Ile Val	
370 375 380	
ggc tcc cac tgc gaa tcc ggc gat atc ctg atc aac gat gaa atc tac	1200
Gly Ser His Cys Glu Ser Gly Asp Ile Leu Ile Asn Asp Glu Ile Tyr	
385 390 395 400	
cca tct gac atc acc agc ggc gac ttc ctt gca ctc gca gcc acc ggc	1248
Pro Ser Asp Ile Thr Ser Gly Asp Phe Leu Ala Leu Ala Ala Thr Gly	
405 410 415	
gca tac tgc tac gcc atg agc tcc cgc tac aac gcc ttc aca cgg ccc	1296
Ala Tyr Cys Tyr Ala Met Ser Ser Arg Tyr Asn Ala Phe Thr Arg Pro	
420 425 430	
gcc gtc gtg tcc gtc cgc gct ggc agc tcc cgc ctc atg ctg cgc cgc	1344
Ala Val Val Ser Val Arg Ala Gly Ser Ser Arg Leu Met Leu Arg Arg	
435 440 445	
gaa acg ctc gac gac atc ctc tca cta gag gca taacgctttt cgaacgctga	1397
Glu Thr Leu Asp Asp Ile Leu Ser Leu Glu Ala	

450

455

ccc

1400

<210> 44
 <211> 459
 <212> FRT
 <213> Corynebacterium glutamicum

<400> 44
 Pro Ala Pro Gly Trp Arg Phe Arg Thr Gly Glu Asp Val Thr Met Ala
 1 5 10 15
 Thr Val Glu Asn Phe Asn Glu Leu Pro Ala His Val Trp Pro Arg Asn
 20 25 30
 Ala Val Arg Gln Glu Asp Gly Val Val Thr Val Ala Gly Val Pro Leu
 35 40 45
 Pro Asp Leu Ala Glu Glu Tyr Gly Thr Pro Leu Phe Val Val Asp Glu
 50 55 60
 Asp Asp Phe Arg Ser Arg Cys Arg Asp Met Ala Thr Ala Phe Gly Gly
 65 70 75 80
 Pro Gly Asn Val His Tyr Ala Ser Lys Ala Phe Leu Thr Lys Thr Ile
 85 90 95
 Ala Arg Trp Val Asp Glu Glu Gly Leu Ala Leu Asp Ile Ala Ser Ile
 100 105 110
 Asn Glu Leu Gly Ile Ala Leu Ala Ala Gly Phe Pro Ala Ser Arg Ile
 115 120 125
 Thr Ala His Gly Asn Asn Lys Gly Val Glu Phe Leu Arg Ala Leu Val
 130 135 140
 Gln Asn Gly Val Gly His Val Val Leu Asp Ser Ala Gln Glu Leu Glu
 145 150 155 160
 Leu Leu Asp Tyr Val Ala Ala Gly Glu Gly Lys Ile Gln Asp Val Leu
 165 170 175
 Ile Arg Val Lys Pro Gly Ile Glu Ala His Thr His Glu Phe Ile Ala
 180 185 190
 Thr Ser His Glu Asp Gln Lys Phe Gly Phe Ser Leu Ala Ser Gly Ser
 195 200 205
 Ala Phe Glu Ala Ala Lys Ala Ala Asn Asn Ala Glu Asn Leu Asn Leu
 210 215 220
 Val Gly Leu His Cys His Val Gly Ser Gln Val Phe Asp Ala Glu Gly
 225 230 235 240
 Phe Lys Leu Ala Ala Glu Arg Val Leu Gly Leu Tyr Ser Gln Ile His
 245 250 255
 Ser Glu Leu Gly Val Ala Leu Pro Glu Leu Asp Leu Gly Gly Gly Tyr
 260 265 270

Gly Ile Ala Tyr Thr Ala Ala Glu Glu Pro Leu Asn Val Ala Glu Val
275 280 285

Ala Ser Asp Leu Leu Thr Ala Val Gly Lys Met Ala Ala Glu Leu Gly
290 295 300

Ile Asp Ala Pro Thr Val Leu Val Glu Pro Gly Arg Ala Ile Ala Gly
305 310 315 320

Pro Ser Thr Val Thr Ile Tyr Glu Val Gly Thr Thr Lys Asp Val His
325 330 335

Val Asp Asp Asp Lys Thr Arg Arg Tyr Ile Ala Val Asp Gly Gly Met
340 345 350

Ser Asp Asn Ile Arg Pro Ala Leu Tyr Gly Ser Glu Tyr Asp Ala Arg
355 360 365

Val Val Ser Arg Phe Ala Glu Gly Asp Pro Val Ser Thr Arg Ile Val
370 375 380

Gly Ser His Cys Glu Ser Gly Asp Ile Leu Ile Asn Asp Glu Ile Tyr
385 390 395 400

Pro Ser Asp Ile Thr Ser Gly Asp Phe Leu Ala Leu Ala Ala Thr Gly
405 410 415

Ala Tyr Cys Tyr Ala Met Ser Ser Arg Tyr Asn Ala Phe Thr Arg Pro
420 425 430

Ala Val Val Ser Val Arg Ala Gly Ser Ser Arg Leu Met Leu Arg Arg
435 440 445

Glu Thr Leu Asp Asp Ile Leu Ser Leu Glu Ala
450 455

<210> 45

<211> 2121

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(2098)

<223> EXA02653

<400> 45

agacagagtg ttagtgogtg gggeagetct caatttcato gacatcactc gagtatgctc 60

accggcogta ttcattccaa taaccgcgac agggaaacta atg ata ccg aag ccc 115
Met ile Pro Lys Pro
1 5

gac gtg acc gac tta tat tta gag gac ctg tta aat gag ggt tcg gaa 163
Asp Val Thr Asp Leu Tyr Leu Glu Asp Leu Leu Asn Glu Gly Ser Glu
10 15 20

aag att cgg tcc gac aag gat ctt tcc gaa ctt agg aca gtt cta aaa 211
Lys ile Arg Ser Ala Lys Asp Leu Ser Glu Leu Arg Thr Val Leu Lys

25	30	35	
gag gtt tcc tcc caa att cag gaa cga gct ggg aaa aaa gat gaa gaa			259
Glu Val Ser Ser Gln Ile Gln Glu Arg Ala Gly Lys Lys Asp Glu Glu			
40	45	50	
tgg gga atg gga gcc aet tgg cgg gag ctg tac ccc agc atc atg gaa			307
Trp Gly Met Gly Ala Thr Trp Arg Glu Leu Tyr Pro Ser Ile Val Glu			
55	60	65	
cgc gct tcc tac gaa ggg cgt gac agc cta atc gga ttt gat cag tta			355
Arg Ala Ser Tyr Glu Gly Arg Asp Ser Leu Ile Gly Phe Asp His Leu			
70	75	80	85
gat cgg gaa atg gaa aga tta gct ttc cgc cca cca tcc gaa agt ttt			403
Ala Arg Glu Met Glu Arg Leu Ala Phe Gly Pro Pro Ser Glu Ser Phe			
90	95	100	
gaa tac ctg cca gaa ctg cta gaa ttc cga ctg gta gac atc aat cag			451
Glu Tyr Leu Gln Glu Leu Val Lys Ser Gly Val Val Asp Ile Thr His			
105	110	115	
ctg aat agt ggt cgg gaa tta ctg ata gat tta gtt cgt gaa att gaa			499
Leu His Arg Gly Arg Glu Ile Leu Thr Asp Leu Val Arg Glu Leu Glu			
120	125	130	
ata aat ctg ctg ata cag gct att att cgt cgg ccc gta gta gta cca			547
Ile Thr Val Val Ile Asp Ala Val Leu Pro Pro Pro Gly Val Val Pro			
135	140	145	
ggc aca ttg ttg cag cag ctg gta aca gag gga tat gac aga atg cgt			595
Gly Thr Leu Val His Asn Leu Val Lys Glu Gly Tyr Ala Arg Met Arg			
150	155	160	165
cct ggg aat cgg ggg tta gat gta gag gct gac ggc aac gtt caa ggg			643
Pro Gly Thr Arg Gly Leu Asp Val Ala Ala Asp Gly Thr Val Gln Gly			
170	175	180	
caa cga cat ttg gct gca ctg gga cgg atg acg gaa gat gtg gtt ttg			691
Gln Arg His Leu Ala Ala Val Gly Arg Met Thr Glu Asp Val Val Leu			
185	190	195	
ggt aat gac aca ttg tgg cga tca tta cat gac ata atc ccc aag tgg			739
Gly Asn Asp Thr Leu Ser Arg Ser Leu His Asp Ile Ile Pro Lys Trp			
200	205	210	
gct cgt cga gtt atc cgc gac gcg agc acg tat ccc gat agg gta cat			787
Ala Arg Arg Val Ile Arg Asp Ala Ser Thr Tyr Pro Asp Arg Val His			
215	220	225	
ggt aat cca ccc att ccc gca cgg ttg gaa ccc tgg gcg gaa aag ctg			835
Gly Thr Pro Pro Leu Pro Ala Arg Leu Glu Pro Trp Ala Glu Lys Leu			
230	235	240	245
aat tca gat ccc gcc aca tgc cgt cag ctg att gaa gaa ttc ggg agt			883
Thr Ser Asp Pro Ala Thr Cys Arg His Leu Ile Glu Glu Phe Gly Ser			
250	255	260	
cct gtg aat gta ctg cat tca ggt tct atg cct cgt aat ata aat gag			931
Pro Val Asn Val Leu His Ser Gly Ser Met Pro Arg Asn Ile Asn Glu			
265	270	275	

ttg gtt gac ggc ggc att cag atg ggg gtg gat act cga ata ttt ttt	979
Leu Val Asp Ala Gly Ile Gln Met Gly Val Asp Thr Arg Ile Phe Phe	
280 285 290	
gac cgc aaa ggc aat aag ggt att acc ttc gtt gat gac gtt aaa gac	1027
Ala Arg Lys Ala Asn Lys Gly Leu Thr Phe Val Asp Ala Val Lys Asp	
295 300 305	
acc agt cat ggt gta gat gta gcc agt gaa cga gag tta tct cag gtg	1075
Thr Gly His Gly Val Asp Val Ala Ser Glu Arg Glu Leu Ser Gln Val	
310 315 320 325	
att aat cgt gga gtc cca gga gag cgg atc att cta tcc gca gct atc	1123
Leu Asn Arg Gly Val Pro Gly Glu Arg Ile Ile Leu Ser Ala Ala Ile	
330 335 340	
aaa cag gac aca cta ttg gca tta cag atc gaa aat ggc ata atc atc	1171
Lys Pro Asp Arg Leu Leu Ala Leu Ala Ile Glu Asn Gly Val Ile Ile	
345 350 355	
tct gtg gat tgg agt gat gaa tta gat cgc att tgg gct ttg gtt agt	1219
Ser Val Asp Ser Arg Asp Glu Leu Asp Arg Ile Ser Ala Leu Val Gly	
360 365 370	
aac cgc att gaa cca att gcc cat aga gta gct cca gat tct gca gtc	1267
Asp Arg Val Ala Arg Val Ala Pro Arg Val Ala Pro Asp Pro Ala Val	
375 380 385	
tta cct cca att aga ttg ggt gag cgt gct gaa gac tgg agt aat cgg	1315
Leu Pro Pro Thr Arg Phe Gly Glu Arg Ala Ala Asp Trp Gly Asn Arg	
390 395 400 405	
att acc gag gtg ata ccc ggc gtg gat att gtg ggt att cag gtt cag	1363
Leu Thr Glu Val Ile Pro Gly Val Asp Ile Val Gly Leu His Val His	
410 415 420	
ctc cat ggc tat gat gca aaa gac cgt gct ctg gct ctg cag gaa tgt	1411
Leu His Gly Tyr Ala Ala Lys Asp Arg Ala Leu Ala Leu Gln Glu Cys	
425 430 435	
tgc caa ctc gtc gat tct ctc aga gaa tgc ggg cat tcc cca cag ttt	1459
Cys Gln Leu Val Asp Ser Leu Arg Glu Cys Gly His Ser Pro Gln Phe	
440 445 450	
att gac att gga gga ggg gtg cct atg agc tac att gaa tct gag gaa	1507
Ile Asp Leu Gly Gly Gly Val Pro Met Ser Tyr Ile Glu Ser Glu Glu	
455 460 465	
gat tgg atc cgt tat caa tcc gct aaa tct gcc act tca gcc ggg tat	1555
Asp Trp Ile Arg Tyr Gln Ser Ala Lys Ser Ala Thr Ser Ala Gly Tyr	
470 475 480 485	
gac gaa tcc ttt acg tgg aaa gac gat ccg tta tct aat acg tac ccg	1603
Ala Glu Ser Phe Thr Trp Lys Asp Asp Pro Leu Ser Asn Thr Tyr Pro	
490 495 500	
ttc tat cag acc cca gtg cgc ggt aat tgg ttg aaa gac gtg att tct	1651
Phe Tyr Gln Thr Pro Val Arg Gly Asn Trp Leu Lys Asp Val Leu Ser	
505 510 515	

aag ggg gta gct cag atg ctc att gac cgg gga atg cgg tta cac ata 1699
 Lys Gly Val Ala Gln Met Leu Ile Asp Arg Gly Leu Arg Leu His Ile
 520 525 530

gag cct ggt cga agt tta cta gat ggg tgt ggc gtc aat att gcc gaa 1747
 Glu Pro Gly Arg Ser Leu Leu Asp Gly Cys Gly Val Thr Leu Ala Glu
 535 540 545

gtt gct ttt gtg aaa acc cga agt gac ggg ttg cct cta gtg gga ctt 1795
 Val Ala Phe Val Lys Thr Arg Ser Asp Gly Leu Pro Leu Val Gly Leu
 550 555 560 565

gct atg aac cga acg cag tgc cgg act aca tcc gat gat ttt ctc att 1843
 Ala Met Asn Arg Thr Gln Cys Arg Thr Thr Ser Asp Asp Phe Leu Ile
 570 575 580

gat gcc ctg cat atc act gac ggt gat gta ggc gag gaa atc gaa gaa 1891
 Asp Pro Leu His Ile Thr Asp Gly Asp Val Gly Glu Glu Ile Glu Ala
 585 590 595

tat cta gtg ggt gcc taa tgc atc gaa gat gag ctg att tta tgc cgg 1939
 Tyr Leu Val Gly Ala Tyr Cys Ile Glu Asp Glu Leu Ile Leu Arg Arg
 600 605 610

cga ctc cgc ttc cag aga gga gtc aaa tca gga gat atc atc gga att 1987
 Arg Ile Arg Phe Pro Arg Gly Val Lys Pro Gly Asp Ile Ile Gly Ile
 615 620 625

cct aac acc gca gga tac ttc atg cat atc ttg gaa agt gaa tgg cac 2035
 Pro Asn Thr Ala Gly Tyr Phe Met His Ile Leu Glu Ser Ala Ser His
 630 635 640 645

caa atc cag ttg ggc aaa cat gta gtg tgg cgg gag ggg cag tta gac 2083
 Gln Ile Pro Leu Ala Lys Asn Val Val Trp Pro Glu Gly Gln Leu Asp
 650 655 660

gat atc gat ggc gat taagacataa ccattcgata atc 2131
 Asp Ile Asp Ala Asp
 665

<210> 46

<211> 666

<212> PRT

<213> Corynebacterium glutamicum

<400> 46

Met Ile Pro Lys Pro Asp Val Thr Asp Leu Tyr Leu Glu Asp Leu Leu
 1 5 10 15

Asn Glu Gly Ser Glu Lys Ile Arg Ser Ala Lys Asp Leu Ser Glu Leu
 20 25 30

Arg Thr Val Leu Lys Glu Val Ser Ser Gln Ile Gln Glu Arg Ala Gly
 35 40 45

Lys Lys Asp Glu Glu Trp Gly Met Gly Ala Thr Trp Arg Glu Leu Tyr
 50 55 60

Pro Ser Ile Val Glu Arg Ala Ser Tyr Glu Gly Arg Asp Ser Leu Ile
 65 70 75 80

Gly	Phe	Asp	His	Leu	Ala	Arg	Glu	Met	Glu	Arg	Leu	Ala	Phe	Gly	Pro
				85					90					95	
Pro	Ser	Glu	Ser	Phe	Glu	Tyr	Leu	Gln	Glu	Leu	Val	Lys	Ser	Gly	Val
			100					105					110		
Val	Asp	Ile	Thr	His	Leu	His	Arg	Gly	Arg	Glu	Pro	Leu	Thr	Asp	Leu
		115					120					125			
Val	Arg	Glu	Leu	Glu	Ile	Thr	Val	Val	Ile	Asp	Ala	Val	Leu	Pro	Pro
		130				135					140				
Pro	Gly	Val	Val	Pro	Gly	Thr	Leu	Val	His	Asn	Leu	Val	Lys	Glu	Gly
145					150					155					160
Tyr	Ala	Arg	Met	Arg	Pro	Gly	Thr	Arg	Gly	Leu	Asp	Val	Ala	Ala	Asp
				165					170					175	
Gly	Thr	Val	Gln	Gly	Gln	Arg	His	Leu	Ala	Ala	Val	Gly	Arg	Met	Thr
		180						185					190		
Glu	Asp	Val	Val	Leu	Gly	Asn	Asp	Thr	Leu	Ser	Arg	Ser	Leu	His	Asp
		195					200					205			
Ile	Ile	Pro	Lys	Trp	Ala	Arg	Arg	Val	Ile	Arg	Asp	Ala	Ser	Thr	Tyr
	210					215					220				
Pro	Asp	Arg	Val	His	Gly	Thr	Pro	Pro	Leu	Pro	Ala	Arg	Leu	Glu	Pro
225					230					235					240
Trp	Ala	Glu	Lys	Leu	Thr	Ser	Asp	Pro	Ala	Thr	Cys	Arg	His	Leu	Ile
				245					250					255	
Glu	Glu	Phe	Gly	Ser	Pro	Val	Asn	Val	Leu	His	Ser	Gly	Ser	Met	Pro
		260						265					270		
Arg	Asn	Ile	Asn	Glu	Leu	Val	Asp	Ala	Gly	Ile	Gln	Met	Gly	Val	Asp
		275					280					285			
Thr	Arg	Ile	Phe	Phe	Ala	Arg	Lys	Ala	Asn	Lys	Gly	Leu	Thr	Phe	Val
	290					295					300				
Asp	Ala	Val	Lys	Asp	Thr	Gly	His	Gly	Val	Asp	Val	Ala	Ser	Glu	Arg
305					310					315					320
Glu	Leu	Ser	Gln	Val	Leu	Asn	Arg	Gly	Val	Pro	Gly	Glu	Arg	Ile	Ile
				325					330					335	
Leu	Ser	Ala	Ala	Ile	Lys	Pro	Asp	Arg	Leu	Leu	Ala	Leu	Ala	Ile	Glu
			340					345					350		
Asn	Gly	Val	Ile	Ile	Ser	Val	Asp	Ser	Arg	Asp	Glu	Leu	Asp	Arg	Ile
		355					360					365			
Ser	Ala	Leu	Val	Gly	Asp	Arg	Val	Ala	Arg	Val	Ala	Pro	Arg	Val	Ala
	370					375					380				
Pro	Asp	Pro	Ala	Val	Leu	Pro	Pro	Thr	Arg	Phe	Gly	Glu	Arg	Ala	Ala
385					390					395					400

Asp Trp Gly Asn Arg Leu Thr Glu Val Ile Pro Gly Val Asp Ile Val
 405 410 415
 Gly Leu His Val His Leu His Gly Tyr Ala Ala Lys Asp Arg Ala Leu
 420 425 430
 Ala Leu Gln Glu Cys Cys Gln Leu Val Asp Ser Leu Arg Glu Cys Gly
 435 440 445
 His Ser Pro Gln Phe Ile Asp Leu Gly Gly Gly Val Pro Met Ser Tyr
 450 455 460
 Ile Glu Ser Glu Glu Asp Trp Ile Arg Tyr Gln Ser Ala Lys Ser Ala
 465 470 475 480
 Thr Ser Ala Gly Tyr Ala Glu Ser Phe Thr Trp Lys Asp Asp Pro Leu
 485 490 495
 Ser Asn Thr Tyr Pro Phe Tyr Gln Thr Pro Val Arg Gly Asn Trp Leu
 500 505 510
 Lys Asp Val Leu Ser Lys Gly Val Ala Gln Met Leu Ile Asp Arg Gly
 515 520 525
 Leu Arg Leu His Ile Glu Pro Gly Arg Ser Leu Leu Asp Gly Cys Gly
 530 535 540
 Val Thr Leu Ala Glu Val Ala Phe Val Lys Thr Arg Ser Asp Gly Leu
 545 550 555 560
 Pro Leu Val Gly Leu Ala Met Asn Arg Thr Gln Cys Arg Thr Thr Ser
 565 570 575
 Asp Asp Phe Leu Ile Asp Pro Leu His Ile Thr Asp Gly Asp Val Gly
 580 585 590
 Glu Glu Ile Glu Ala Tyr Leu Val Gly Ala Tyr Cys Ile Glu Asp Glu
 595 600 605
 Leu Ile Leu Arg Arg Arg Ile Arg Phe Pro Arg Gly Val Lys Pro Gly
 610 615 620
 Asp Ile Ile Gly Ile Pro Asn Thr Ala Gly Tyr Phe Met His Ile Leu
 625 630 635 640
 Glu Ser Ala Ser His Gln Ile Pro Leu Ala Lys Asn Val Val Trp Pro
 645 650 655
 Glu Gly Gln Leu Asp Asp Ile Asp Ala Asp
 660 665

<210> 47
 <211> 993
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(970)
 <223> RXA01393

<400> 47

caaaaagcaga cctgtaatga agatttccat gatcaccatc gtagcctatg gaagtactta 60
 agtaaaatga ttgggttetta acatgggtta atatagettic atg aac ccc att caa 115
 Met Asn Pro Ile Gln
 1 5
 ctg gac aat ttg ctc tca atc att gat gaa ggc agc ttc gaa ggc gcc 163
 Leu Asp Thr Leu Leu Ser Ile Ile Asp Glu Gly Ser Phe Glu Gly Ala
 10 15 20
 tcc tta gcc ctt tcc att tcc ccc tgg ggc gtg agt cag cgc gtt aaa 211
 Ser Leu Ala Leu Ser Ile Ser Pro Ser Ala Val Ser Gln Arg Val Lys
 25 30 35
 gat ctc gag cat ccc gtg ggt cga gta ttc gta tgg cgc arg caa tgg 259
 Ala Leu Glu His His Val Gly Arg Val Leu Val Ser Arg Thr Gln Pro
 40 45 50
 gac aac gca aac gaa ggc ggt gaa gta ttc gtg caa cca ggc tgg caa 307
 Ala Lys Ala Thr Glu Ala Gly Glu Val Leu Val Gln Ala Ala Arg Lys
 55 60 65
 atg gtg ttg ctg caa gca gaa aat aac gag caa tta tct gga cgc att 365
 Met Val Leu Leu Gln Ala Glu Thr Lys Ala Gln Leu Ser Gly Arg Leu
 70 75 80
 gat gaa atc cgc tta acc atc gcc atc aac gaa gat tgg cta tcc aca 403
 Ala Glu Ile Pro Leu Thr Ile Ala Ile Asn Ala Asp Ser Leu Ser Thr
 85 90 95
 tgg ttt cct ccc gtg ttc aac gag gta gct tct tgg ggt gga gca acg 461
 Trp Phe Pro Pro Val Phe Asn Glu Val Ala Ser Trp Gly Gly Ala Thr
 105 110 115
 ctc acg ctg cgc ttg gaa gat gaa ggc cac aca tta tcc ttg ctg cgg 499
 Leu Thr Leu Arg Leu Glu Asp Glu Ala His Thr Leu Ser Leu Leu Arg
 120 125 130
 cgt gga gat gtt tta gga ggc gta aac cgt gaa gct aat ccc gtg ggc 547
 Arg Gly Asp Val Leu Gly Ala Val Thr Arg Glu Ala Asn Pro Val Ala
 135 140 145
 gga tgt gaa gta gta gaa ctt gga acc atg cgc cac ttg gcc att gca 595
 Gly Cys Glu Val Val Glu Leu Gly Thr Met Arg His Leu Ala Ile Ala
 150 155 160 165
 acc ccc tca ttg cgg gat gcc tac atg gtt gat ggg aaa cta gat tgg 643
 Thr Pro Ser Leu Arg Asp Ala Tyr Met Val Asp Gly Lys Leu Asp Trp
 170 175 180
 gct ggc atg ccc gtc tta cgc ttc ggt ccc aaa gat gtg ctt caa gac 691
 Ala Ala Met Pro Val Leu Arg Phe Gly Pro Lys Asp Val Leu Gln Asp
 185 190 195
 cgt gac ctg gac ggg cgc gtc gat ggt cct gtg ggg cgc agg cgc gta 739
 Arg Asp Leu Asp Gly Arg Val Asp Gly Pro Val Gly Arg Arg Arg Val
 200 205 210
 tcc att gtc ccg tgg ggc gaa ggt ttt ggt gag gca att cgc cga ggc 787

Ser Ile Val Pro Ser Ala Glu Gly Phe Gly Glu Ala Ile Arg Arg Gly
 215 220 225

ctt ggt tgg gga ctt ctt ccc gaa acc caa gct gct ccc atg cta aaa 835
 Leu Gly Trp Gly Leu Leu Pro Glu Thr Gln Ala Ala Pro Met Leu Lys
 230 235 240 245

gca gga gaa gtg atc ctc ctc gat gag ata ccc att gac aca cgg atg 885
 Ala Gly Glu Val Ile Leu Leu Asp Glu Ile Pro Ile Asp Thr Pro Met
 250 255 260

tat tgg caa cga tgg cgt ctg gaa tct aga tct cta gct aga ctc aca 935
 Tyr Trp Gln Arg Trp Arg Leu Glu Ser Arg Ser Leu Ala Arg Leu Thr
 265 270 275

gac gac gtc gtt gat gaa gaa atc gag gga tgg agt cct tgg tacttc 985
 Asp Ala Val Val Asp Ala Ala Ile Glu Gly Leu Arg Pro
 280 285 290

taaaaggtt cag 995

<210> 48
 <211> (39)
 <212> PRT
 <213> Corynebacterium glutamicum

<40> 48
 Met Asn Pro Ile Gln Leu Asp Thr Leu Leu Ser Ile Ile Asp Glu Gly
 1 5 10 15

Ser Phe Glu Gly Ala Ser Leu Ala Leu Ser Ile Ser Pro Ser Ala Val
 20 25 30

Ser Gln Arg Val Lys Ala Leu Glu His His Val Gly Arg Val Leu Val
 35 40 45

Ser Arg Thr Gln Pro Ala Lys Ala Thr Glu Ala Gly Glu Val Leu Val
 50 55 60

Gln Ala Ala Arg Lys Met Val Leu Leu Gln Ala Glu Thr Lys Ala Gln
 65 70 75 80

Leu Ser Gly Arg Leu Ala Glu Ile Pro Leu Thr Ile Ala Ile Asn Ala
 85 90 95

Asp Ser Leu Ser Thr Trp Phe Pro Pro Val Phe Asn Glu Val Ala Ser
 100 105 110

Trp Gly Gly Ala Thr Leu Thr Leu Arg Leu Glu Asp Glu Ala His Thr
 115 120 125

Leu Ser Leu Leu Arg Arg Gly Asp Val Leu Gly Ala Val Thr Arg Glu
 130 135 140

Ala Asn Pro Val Ala Gly Cys Glu Val Val Glu Leu Gly Thr Met Arg
 145 150 155 160

His Leu Ala Ile Ala Thr Pro Ser Leu Arg Asp Ala Tyr Met Val Asp
 165 170 175

Gly Lys Leu Asp Trp Ala Ala Met Pro Val Leu Arg Phe Gly Pro Lys
180 185 190

Asp Val Leu Gln Asp Arg Asp Leu Asp Gly Arg Val Asp Gly Pro Val
195 200 205

Gly Arg Arg Arg Val Ser Ile Val Pro Ser Ala Glu Gly Phe Gly Glu
210 215 220

Ala Ile Arg Arg Gly Leu Gly Trp Gly Leu Leu Pro Glu Thr Gln Ala
225 230 235 240

Ala Pro Met Leu Lys Ala Gly Glu Val Ile Leu Leu Asp Glu Ile Pro
245 250 255

Ile Asp Thr Pro Met Tyr Trp Gln Arg Trp Arg Leu Glu Ser Arg Ser
260 265 270

Leu Ala Arg Leu Thr Asp Ala Val Val Asp Ala Ala Ile Glu Gly Leu
275 280 285

Arg Pro
290

<210> 49
<211> 1626
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1603)
<223> RNA30241

<400> 49
ggtcttcagc atttataaac aatttcattcg cacttgattt attggcccca agattacggg 60

aagtttagcg aatttcgcgt acgtcaacta cgttaaata gtg aat act caa tca 115
Val Asn Thr Gln Ser
1 5

gat tct ggg ggg tct caa ggt gca ggg gcc aca agt cgt act gta tct 163
Asp Ser Ala Gly Ser Gln Gly Ala Ala Ala Thr Ser Arg Thr Val Ser
10 15 20

att aga acc ctg atc ggg ctg atc atc gga tgg acc gtc ggc gcg gga 211
Ile Arg Thr Leu Ile Ala Leu Ile Ile Gly Ser Thr Val Gly Ala Gly
25 30 35

att ttc tcc atc cct caa aac atc ggc tca gtc gca ggt ccc ggc gcg 259
Ile Phe Ser Ile Pro Gln Asn Ile Gly Ser Val Ala Gly Pro Gly Ala
40 45 50

atg ctg atc ggc tgg ctg atc gcc ggt gtg ggc atg ttg tcc gta gcg 307
Met Leu Ile Gly Trp Leu Ile Ala Gly Val Gly Met Leu Ser Val Ala
55 60 65

ttc ggg ttc cat gtt ctt gcc cgc cgt aaa cct caa ctg gat tct ggc 355
Phe Val Phe His Val Leu Ala Arg Arg Lys Pro His Leu Asp Ser Gly
70 75 80 85

gtc tac gca tat ggc cgt gtt gga ttg ggc gat tat gta ggt ttc tcc	403
Val Tyr Ala Tyr Ala Arg Val Gly Leu Gly Asp Tyr Val Gly Phe Ser	
90 95 100	
cac gct tgg ggt tat tgg ctg ggt tca gtc atc gcc caa gtt ggc tac	451
Ser Ala Trp Gly Tyr Trp Leu Gly Ser Val Ile Ala Gln Val Gly Tyr	
105 110 115	
gca acg tta ttt ttc tcc acg ttg ggc cac tac gta cag ctg ttt tcc	499
Ala Thr Leu Phe Phe Ser Thr Leu Gly His Tyr Val Pro Leu Phe Ser	
120 125 130	
caa gat cat caa ttt gtg tca ggc ttg gca gtt agc ggt ttg acc tgg	547
Gln Asp His Pro Phe Val Ser Ala Leu Ala Val Ser Ala Leu Thr Trp	
135 140 145	
ctg gtg ttt gga gtt gtt tcc cga gga att agc caa ggt ggt ttc ttg	595
Leu Val Phe Gly Val Val Ser Arg Gly Ile Ser Gln Ala Ala Phe Leu	
150 155 160 165	
ata acg gtc acc acc gtg ggt aaa att ctg gtt ctg ttg tgc ttc att	643
Thr Thr Val Thr Thr Val Ala Lys Ile Leu Pro Leu Leu Cys Phe Ile	
170 175 180	
atc att gtt gca ttc ttc ggc ttt agt tgg gag aag ttc act gtt gat	691
Ile Leu Val Ala Phe Leu Gly Phe Ser Trp Glu Lys Phe Thr Val Asp	
185 190 195	
tta tgg ggc cgt gat ggt ggc gtg ggc agc att ttt gat cac gtg ggc	739
Leu Trp Ala Arg Asp Gly Gly Val Gly Ser Ile Phe Asp Gln Val Arg	
200 205 210	
ggc atc atg gtg tac acc ctg tgg gtg ttc atc ggt atc gaa ggt gca	787
Gly Ile Met Val Tyr Thr Val Trp Val Phe Ile Gly Ile Glu Gly Ala	
215 220 225	
tcg gta tat tcc cgc cag gca cgc tca cgc agt gat gtc agc cga gct	835
Ser Val Tyr Ser Arg Gln Ala Arg Ser Arg Ser Asp Val Ser Arg Ala	
230 235 240 245	
acc gtg att ggt ttt gtg gct gtt ctc ctt ttg ctg gtg tgg att tat	883
Thr Val Ile Gly Phe Val Ala Val Leu Leu Leu Val Ser Ile Ser	
250 255 260	
tcg ctg agc ttc ggt gta ctg acc caa caa gag ctc gct gcc tta cca	931
Ser Leu Ser Phe Gly Val Leu Thr Gln Gln Glu Leu Ala Ala Leu Pro	
265 270 275	
gat aat tcc atg ggc tgc gtg ctc gaa gct gtt gtt ggt cca tgg ggt	979
Asp Asn Ser Met Ala Ser Val Leu Glu Ala Val Val Gly Pro Trp Gly	
280 285 290	
gcc gca ttg att tgc ttg ggt ctg tgt ctt tgc gtt ctt ggc gcc tat	1027
Ala Ala Leu Ile Ser Leu Gly Leu Cys Leu Ser Val Leu Gly Ala Tyr	
295 300 305	
gtg tcc tgg cag atg ctc tgc gca gaa cca ctg gcc ttg atg gca atg	1075
Val Ser Trp Gln Met Leu Cys Ala Glu Pro Leu Ala Leu Met Ala Met	
310 315 320 325	

gat ggc ctc att cca agc aaa atc ggg gcc atc aac agc cgc ggt gct 1123
 Asp Gly Leu Ile Pro Ser Lys Ile Gly Ala Ile Asn Ser Arg Gly Ala
 330 335 340

gcc tgg atg gct cag ctg atc tcc acc atc gtg att cag att ttc atc 1171
 Ala Trp Met Ala Gln Leu Ile Ser Thr Ile Val Ile Gln Ile Phe Ile
 345 350 355

atc att ttc ttc ctc aac gag acc acc tac gtc tcc atg gtg caa ttg 1219
 Ile Ile Phe Phe Leu Asn Glu Thr Thr Tyr Val Ser Met Val Gln Leu
 360 365 370

gct acc aac cta tac ttg gtg cct tac ctg ttc tct gcc ttt tat ctg 1267
 Ala Thr Asn Leu Tyr Leu Val Pro Tyr Leu Phe Ser Ala Phe Tyr Leu
 375 380 385

gtc atg atg gga acc cgt gga aaa gga atc acc cag acc cat gtc gtc 1315
 Val Met Leu Ala Thr Arg Gly Lys Gly Ile Thr His Pro His Ala Gly
 390 395 400 405

aca cgt ttc gat gat tcc ggt cca gag ata ttc cgc cga gaa aac cgc 1363
 Thr Arg Phe Asp Asp Ser Gly Pro Glu Ile Ser Arg Arg Glu Asn Arg
 410 415 420

aaa cac ctc atc gtc ggt tta gta gaa acc gtg tat tca gtg tgg ctg 1411
 Lys His Leu Ile Val Gly Leu Val Ala Thr Val Tyr Ser Val Trp Leu
 425 430 435

tat tac ggt gga gaa cag cag ttt gtc atc ttc gaa gcc atc gag atg 1459
 Phe Tyr Ala Ala Glu Pro Gln Phe Val Leu Phe Gly Ala Met Ala Met
 440 445 450

ctt acc ggc tta atc ccc tat ggc tgg acc agg att tat gtc ggc gaa 1507
 Leu Pro Gly Leu Ile Pro Tyr Val Trp Thr Arg Ile Tyr Arg Gly Glu
 455 460 465

cag gtg ttt aac cgc ttt gaa atc ggc gtg gtt gtt gtc ctg gtc gct 1555
 Gln Val Phe Asn Arg Phe Glu Ile Gly Val Val Val Val Leu Val Val
 470 475 480 485

gct gcc agc ggc ggc gtt att ggt ttg gtc aac gga tca cta tgg ctt 1603
 Ala Ala Ser Ala Gly Val Ile Gly Leu Val Asn Gly Ser Leu Ser Leu
 490 495 500

taaacaccca aaccttccctg cta 1626

<210> 50
 <211> 501
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 50
 Val Asn Thr Gln Ser Asp Ser Ala Gly Ser Gln Gly Ala Ala Ala Thr
 1 5 10 15
 Ser Arg Thr Val Ser Ile Arg Thr Leu Ile Ala Leu Ile Ile Gly Ser
 20 25 30
 Thr Val Gly Ala Gly Ile Phe Ser Ile Pro Gln Asn Ile Gly Ser Val
 35 40 45

Ala Gly Pro Gly Ala Met Leu Ile Gly Trp Leu Ile Ala Gly Val Gly
 50 55 60
 Met Leu Ser Val Ala Phe Val Phe His Val Leu Ala Arg Arg Lys Pro
 65 70 75 80
 His Leu Asp Ser Gly Val Tyr Ala Tyr Ala Arg Val Gly Leu Gly Asp
 85 90 95
 Tyr Val Gly Phe Ser Ser Ala Trp Gly Tyr Trp Leu Gly Ser Val Ile
 100 105 110
 Ala Gln Val Gly Tyr Ala Thr Leu Phe Phe Ser Thr Leu Gly His Tyr
 115 120 125
 Val Pro Leu Phe Ser Gln Asp His Pro Phe Val Ser Ala Leu Ala Val
 130 135 140
 Ser Ala Leu Thr Trp Leu Val Phe Gly Val Val Ser Arg Gly Ile Ser
 145 150 155 160
 Gln Ala Ala Phe Leu Thr Thr Val Thr Thr Val Ala Lys Ile Leu Pro
 165 170 175
 Leu Leu Cys Phe Ile Ile Leu Val Ala Phe Leu Gly Ile Ser Trp Gln
 180 185 190
 Lys Ile Thr Val Asp Leu Trp Ala Arg Asp Gly Gly Val Gly Ser Ile
 195 200 205
 Phe Asp Gln Val Arg Gly Ile Met Val Tyr Thr Val Trp Val Phe Ile
 210 215 220
 Gly Ile Glu Gly Ala Ser Val Tyr Ser Arg Gln Ala Arg Ser Arg Ser
 225 230 235 240
 Asp Val Ser Arg Ala Thr Val Ile Gly Phe Val Ala Val Leu Leu Leu
 245 250 255
 Leu Val Ser Ile Ser Ser Leu Ser Phe Gly Val Leu Thr Gln Gln Glu
 260 265 270
 Leu Ala Ala Leu Pro Asp Asn Ser Met Ala Ser Val Leu Glu Ala Val
 275 280 285
 Val Gly Pro Trp Gly Ala Ala Leu Ile Ser Leu Gly Leu Cys Leu Ser
 290 295 300
 Val Leu Gly Ala Tyr Val Ser Trp Gln Met Leu Cys Ala Glu Pro Leu
 305 310 315 320
 Ala Leu Met Ala Met Asp Gly Leu Ile Pro Ser Lys Ile Gly Ala Ile
 325 330 335
 Asn Ser Arg Gly Ala Ala Trp Met Ala Gln Leu Ile Ser Thr Ile Val
 340 345 350
 Ile Gln Ile Phe Ile Ile Ile Phe Phe Leu Asn Glu Thr Thr Tyr Val
 355 360 365

Ser Met Val Gln Leu Ala Thr Asn Leu Tyr Leu Val Pro Tyr Leu Phe
370 375 380

Ser Ala Phe Tyr Leu Val Met Leu Ala Thr Arg Gly Lys Gly Ile Thr
385 390 395 400

His Pro His Ala Gly Thr Arg Phe Asp Asp Ser Gly Pro Glu Ile Ser
405 410 415

Arg Arg Glu Asn Arg Lys His Leu Ile Val Gly Leu Val Ala Thr Val
420 425 430

Tyr Ser Val Trp Leu Phe Tyr Ala Ala Glu Pro Gln Phe Val Leu Phe
435 440 445

Gly Ala Met Ala Met Leu Pro Gly Leu Ile Pro Tyr Val Trp Thr Arg
450 455 460

Ile Tyr Arg Gly Glu Gln Val Phe Asn Arg Phe Glu Ile Gly Val Val
465 470 475 480

Val Val Leu Val Val Ala Ala Ser Ala Gly Val Ile Gly Leu Val Asn
485 490 495

Gly Ser Leu Ser Leu
500

<210> 51

<211> 822

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)...(799)

<223> RXA01394

<400> 51

gagcaaaagtg tccagttgaa tgggggttcac gaagctatat taaaccatgt taagaaccaa 60

ccattttact taagtacttc cataggtcac gatgggtgac atg gaa atc ttc att 115
Met Glu Ile Phe Ile
1 5

aca ggt ctg ctt ttg ggg gcc agt ctt tta ctg tcc atc gga ccg caa 163
Thr Gly Leu Leu Leu Gly Ala Ser Leu Leu Leu Ser Ile Gly Pro Gln
10 15 20

aat gta ctg gtg att aaa caa gga att aag cgc gaa gga ctc att gcg 211
Asn Val Leu Val Ile Lys Gln Gly Ile Lys Arg Glu Gly Leu Ile Ala
25 30 35

gtt ctt ctc gtg tgt tta att tct gac gtc ttt ttg ttc atc gcc gcc 259
Val Leu Leu Val Cys Leu Ile Ser Asp Val Phe Leu Phe Ile Ala Gly
40 45 50

acc ttg gcc gtt gat ctt ttg tcc aat gcc gcc ccg atc gtg ctc gat 307
Thr Leu Gly Val Asp Leu Leu Ser Asn Ala Ala Pro Ile Val Leu Asp
55 60 65

att atg cgc tgg ggt ggc atc gct tac ctg tta tgg ttt gcc gtc atg 355
 Ile Met Arg Trp Gly Gly Ile Ala Tyr Leu Leu Trp Phe Ala Val Met
 70 75 80 85

 gca gcg aaa gac gcc atg aca aac aag qtg gaa gcg cca cag atc att 403
 Ala Ala Lys Asp Ala Met Thr Asn Lys Val Glu Ala Pro Gln Ile Ile
 90 95 100

 gaa gaa aca gaa cca acc gtg ccc gat gac acg cct ttg gcc ggt tgg 451
 Glu Glu Thr Glu Pro Thr Val Pro Asp Asp Thr Pro Leu Gly Gly Ser
 105 110 115

 gag gtg gcc acg gac acg cgc aac cgg gtg cgg gtg gag gtg agc gtc 499
 Ala Val Ala Thr Asp Thr Arg Asn Arg Val Arg Val Glu Val Ser Val
 120 125 130

 gat aag aag cgg gtt tgg gta aag ccc atg ttg atg gca atc tgg ctg 547
 Asp Lys Gln Arg Val Trp Val Lys Pro Met Leu Met Ala Ile Val Leu
 135 140 145

 acc tgg ttg aac cgg aat ggg tac ttt gac gcg ttt gtg ttt atc gcc 595
 Thr Trp Leu Asn Pro Asn Ala Tyr Leu Asp Ala Phe Val Phe Ile Gly
 150 155 160 165

 ggc gtc gcc gcg caa tac gcc gac aac gga cgg tgg att ttc gcc gct 643
 Gly Val Gly Ala Gln Tyr Gly Asp Thr Gly Arg Trp Ile Phe Ala Ala
 170 175 180

 ggc gag tta ggg gta agc atg atc tgg ttt cgg atg gtg gtt ttc gcc 691
 Gly Ala Phe Ala Ala Ser Leu Ile Trp Phe Pro Leu Val Gly Phe Gly
 185 190 195

 gca gca gca tgg aca gcc cgg atg ttt agc ccc aag gtg ttt gcc tgg 739
 Ala Ala Ala Leu Ser Arg Pro Leu Ser Ser Pro Lys Val Trp Arg Trp
 200 205 210

 atc aac gtc gtc gtg gca gtt gtg atg acc gca ttg gcc atc aaa ctg 787
 Ile Asn Val Val Val Ala Val Val Met Thr Ala Leu Ala Ile Lys Leu
 215 220 225

 atg ttg atg ggt tagttttcgc gggttttgga atc 822
 Met Leu Met Gly
 230

<210> 52

<211> 233

<212> PRT

<213> Corynebacterium glutamicum

<400> 52

Met Glu Ile Phe Ile Thr Gly Leu Leu Leu Gly Ala Ser Leu Leu Leu
 1 5 10 15

Ser Ile Gly Pro Gln Asn Val Leu Val Ile Lys Gln Gly Ile Lys Arg
 20 25 30

Glu Gly Leu Ile Ala Val Leu Leu Val Cys Leu Ile Ser Asp Val Phe
 35 40 45

Leu Phe Ile Ala Gly Thr Leu Gly Val Asp Leu Leu Ser Asn Ala Ala

50

55

60

Pro Ile Val Leu Asp Ile Met Arg Trp Gly Gly Ile Ala Tyr Leu Leu
65 70 75 80

Trp Phe Ala Val Met Ala Ala Lys Asp Ala Met Thr Asn Lys Val Glu
85 90 95

Ala Pro Gln Ile Ile Glu Glu Thr Glu Pro Thr Val Pro Asp Asp Thr
100 105 110

Pro Leu Gly Gly Ser Ala Val Ala Thr Asp Thr Arg Asn Arg Val Arg
115 120 125

Val Glu Val Ser Val Asp Lys Gln Arg Val Trp Val Lys Pro Met Leu
130 135 140

Met Ala Ile Val Leu Thr Trp Leu Asn Pro Asn Ala Tyr Leu Asp Ala
145 150 155 160

Phe Val Phe Ile Gly Gly Val Gly Ala Gln Tyr Gly Asp Thr Gly Arg
165 170 175

Trp Ile Phe Ala Ala Gly Ala Phe Ala Ala Ser Leu Ile Trp Phe Pro
180 185 190

Leu Val Gly Phe Gly Ala Ala Ala Leu Ser Arg Pro Leu Ser Ser Pro
195 200 205

Lys Val Trp Arg Trp Ile Asn Val Val Val Ala Val Val Met Thr Ala
210 215 220

Leu Ala Ile Lys Leu Met Leu Met Gly
225 230

<210> 53

<211> 1326

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1003)

<223> RXA00865

<400> 53

ttatcggaat gtggttggg cgattgttat gcaaaagttg ttaggttttt tgcgggggttg 60

tttaaccccc aaatgagggga agaaggtaac ctggaactct atg agc aca ggt tta 115
Met Ser Thr Gly Leu
1 5

aca gct aag acc gga gta gag cac ttc ggc acc gtt gga gta gca atg 163
Thr Ala Lys Thr Gly Val Glu His Phe Gly Thr Val Gly Val Ala Met
10 15 20

gtt act cca ttc acg gaa tcc gga gac atc gat atc gct gct ggc cgc 211
Val Thr Pro Phe Thr Glu Ser Gly Asp Ile Asp Ile Ala Ala Gly Arg
25 30 35

gaa gtc geg get tat ttg gtt gat aag ggc ttg gat tct atg gtt ctc	259
Glu Val Ala Ala Tyr Leu Val Asp Lys Gly Leu Asp Ser Leu Val Leu	
40 45 50	
ggg ggc acc act ggt gaa tcc cca aag aca aac ggc get gaa aia cta	307
Ala Gly Thr Thr Gly Glu Ser Pro Thr Thr Thr Ala Ala Glu Lys Leu	
55 60 65	
gaa ctg ctg aag gac gtt cgt gag gaa gtt ggg gat cgg ggc aag ctg	355
Glu Leu Leu Lys Ala Val Arg Glu Glu Val Gly Asp Arg Ala Lys Leu	
70 75 80 85	
atc gac gat gtc gga acc aac aac aag cgg aca tat gtg gaa ctt ggc	403
Ile Ala Gly Val Gly Thr Asn Asn Thr Arg Thr Ser Val Glu Leu Ala	
90 95 100	
gaa ggt gtt gtt tat ggt ggt gaa gat gat ttt tta att gta act cct	451
Glu Ala Ala Ala Ser Ala Gly Ala Asp Gly Leu Leu Val Val Thr Pro	
105 110 115	
tat tac tcc aag ccc acc caa gag gga tta ctg ggc cac tta gat gaa	499
Tyr Tyr Ser Lys Pro Ser Gln Glu Gly Leu Leu Ala His His Gly Ala	
120 125 130	
att get gaa gaa aca gag gtt cca att tgt cta tat gac att cct ggt	547
Ile Ala Ala Ala Thr Glu Val Pro Ile Cys Leu Tyr Asp Ile Pro Gly	
135 140 145	
agg tca ggt att cct att gag tat gat att atg aca cgc ctg att gaa	595
Arg Ser Gly Ile Pro Ile Glu Ser Asp Thr Met Arg Arg Leu Ser Glu	
150 155 160 165	
tta ctt att att ttg ggc gtc aag gac ggc aag ggt gat ctg att gaa	643
Leu Pro Thr Ile Leu Ala Val Lys Asp Ala Lys Gly Asp Leu Val Ala	
170 175 180	
ggc aag tca ttg atc aaa gaa acg gga ctt gtc tgg tat tca ggc gat	691
Ala Thr Ser Leu Ile Lys Glu Thr Gly Leu Ala Trp Tyr Ser Gly Asp	
185 190 195	
gac cca cta aac ctt gtt tgg ctt gat ttg ggc gga tca ggt ttc att	739
Asp Pro Leu Asn Leu Val Trp Leu Ala Leu Gly Gly Ser Gly Phe Ile	
200 205 210	
tcc gta att gga cat gca gcc ccc aca gca tta cgt gag ttg tac aca	787
Ser Val Ile Gly His Ala Ala Pro Thr Ala Leu Arg Glu Leu Tyr Thr	
215 220 225	
agc ttc gag gaa ggc gac ctc gtc cgt gcg cgg gaa atc aac gcc aaa	835
Ser Phe Glu Glu Gly Asp Leu Val Arg Ala Arg Glu Ile Asn Ala Lys	
230 235 240 245	
cta tca ccc ctg gta get gcc caa ggt cgc ttg ggt gga gtc agc ttg	883
Leu Ser Pro Leu Val Ala Ala Gln Gly Arg Leu Gly Gly Val Ser Leu	
250 255 260	
gaa aaa gtt gtt ctg cgt ctg cag ggc atc aac gta gga gat cct cga	931
Ala Lys Ala Ala Leu Arg Leu Gln Gly Ile Asn Val Gly Asp Pro Arg	
265 270 275	
ctt cca att atg gtt cca aat gag cag gaa att gag gat ctc cga gaa	979

Leu Pro Ile Met Ala Pro Asn Glu Gln Glu Leu Glu Ala Leu Arg Glu
 280 285 290

gac atg aaa aaa gct gga gtt cta taaatatgaa tgattccaga aat 1026
 Asp Met Lys Lys Ala Gly Val Leu
 295 300

<210> 54
 <211> 301
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 54
 Met Ser Thr Gly Leu Thr Ala Lys Thr Gly Val Glu His Phe Gly Thr
 1 5 10 15

Val Gly Val Ala Met Val Thr Pro Phe Thr Glu Ser Gly Asp Ile Asp
 20 25 30

Ile Ala Ala Gly Arg Glu Val Ala Ala Tyr Leu Val Asp Lys Gly Leu
 35 40 45

Asp Ser Leu Val Leu Ala Gly Thr Thr Gly Glu Ser Pro Thr Thr Thr
 50 55 60

Ala Ala Glu Lys Leu Gln Leu Leu Lys Ala Val Arg Glu His Val Gly
 65 70 75 80

Asp Arg Ala Lys Leu Ile Ala Gly Val Gly Thr Asn Asn Thr Arg Thr
 85 90 95

Ser Val Glu Leu Ala Glu Ala Ala Ala Ser Ala Gly Ala Asp Gly Leu
 100 105 110

Leu Val Val Thr Pro Tyr Tyr Ser Lys Pro Ser Gln Glu Gly Leu Leu
 115 120 125

Ala His Phe Gly Ala Ile Ala Ala Ala Thr Glu Val Pro Ile Cys Leu
 130 135 140

Tyr Asp Ile Pro Gly Arg Ser Gly Ile Pro Ile Glu Ser Asp Thr Met
 145 150 155 160

Arg Arg Leu Ser Glu Leu Pro Thr Ile Leu Ala Val Lys Asp Ala Lys
 165 170 175

Gly Asp Leu Val Ala Ala Thr Ser Leu Ile Lys Glu Thr Gly Leu Ala
 180 185 190

Trp Tyr Ser Gly Asp Asp Pro Leu Asn Leu Val Trp Leu Ala Leu Gly
 195 200 205

Gly Ser Gly Phe Ile Ser Val Ile Gly His Ala Ala Pro Thr Ala Leu
 210 215 220

Arg Glu Leu Tyr Thr Ser Phe Glu Glu Gly Asp Leu Val Arg Ala Arg
 225 230 235 240

Glu Ile Asn Ala Lys Leu Ser Pro Leu Val Ala Ala Gln Gly Arg Leu
 245 250 255

Gly Gly Val Ser Leu Ala Lys Ala Ala Leu Arg Leu Gln Gly Ile Asn
260 265 270

Val Gly Asp Pro Arg Leu Pro Ile Met Ala Pro Asn Glu Gln Glu Leu
275 280 285

Glu Ala Leu Arg Glu Asp Met Lys Lys Ala Gly Val Leu
290 295 300

<210> 55

<211> 1071

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (131)...(104-)

<223> RXS02011

<400> 55

tggggggggg gaggagatc aatctgtt tgaatcaga gtcacaggt ttaacata 60

aaacottagt taaacatga tggagggg agataaaa atg agt gaa tac att 115
Met Ser Glu Asn Ile
1 5

ggt gga gtt aag gta att ggt atc gaa aat att ggt att gaa ggg aat 163
Arg Gly Ala Gln Ala Val Gly Ile Ala Asn Ile Ala Met Asp Gly Thr
10 15 20

atc ctg gac aag tgg tac cca gaa ccc caa att ttc aac ctg gat cag 211
Ile Leu Asp Thr Trp Tyr Pro Glu Pro Gln Ile Phe Asn Pro Asp Gln
25 30 35

tgg gct gaa cgc tac cca ttg gaa gtg ggc acc aca cgc ctg gga gaa 259
Trp Ala Glu Arg Tyr Pro Leu Glu Val Gly Thr Thr Arg Leu Gly Ala
40 45 50

aac gaa ctg acc cca cgg atg ctg cag ttg gta aaa ctg gac caa gat 307
Asn Glu Leu Thr Pro Arg Met Leu Gln Leu Val Lys Leu Asp Gln Asp
55 60 65

cgc ctg gtc gaa cag gta gaa gtc cgc acc gtt atc ccc gat ctg tct 355
Arg Leu Val Glu Gln Val Ala Val Arg Thr Val Ile Pro Asp Leu Ser
70 75 80 85

caa cct cca gta gac gcg cac gat gtt tac ctg cgc ctg cac ctg ctt 403
Gln Pro Pro Val Asp Ala His Asp Val Tyr Leu Arg Leu His Leu Leu
90 95 100

tcc cac cgg ctg gtc cgc ccc cac gaa atg cac atg caa aac acc ttg 451
Ser His Arg Leu Val Arg Pro His Glu Met His Met Gln Asn Thr Leu
105 110 115

gag ctg ctg tcc gac ggg ggg tgg aca aac aag ggc cct tgc ctt cct 499
Glu Leu Leu Ser Asp Val Val Trp Thr Asn Lys Gly Pro Cys Leu Pro
120 125 130

gaa aac ttt gag tgg gtc ggt ggt gct ctg cgg tcc cgc gga ctg atc 547

Glu Asn Phe Glu Trp Val Arg Gly Ala Leu Arg Ser Arg Gly Leu Ile
 135 140 145

cac gtc tac tgt gtg gac cgt ctt ccc cgc atg gtc gac tat gtg gtt 595
 His Val Tyr Cys Val Asp Arg Leu Pro Arg Met Val Asp Tyr Val Val
 150 155 160 165

ccc cct gga gtc cgc atc tcc gaa gca gaa cgc gtg cgc cta ggt gca 643
 Pro Pro Gly Val Arg Ile Ser Glu Ala Glu Arg Val Arg Leu Gly Ala
 170 175 180

tac att gct ccg ggt acc tct gtg ctg cgt gaa ggt ttc gtg tct ttc 691
 Tyr Leu Ala Pro Gly Thr Ser Val Leu Arg Glu Gly Phe Val Ser Phe
 185 190 195

aac tcc ggc acc ttg ggt gac gca aag gtg gaa ggc cgc atg agt tcc 739
 Asn Ser Gly Thr Leu Gly Ala Ala Lys Val Glu Gly Arg Leu Ser Ser
 200 205 210

ggt gtg atc atc ggt gaa ggt tcc aac att gga ctg tct tct act att 787
 Gly Val Val Ile Gly Glu Gly Ser Glu Ile Gly Leu Ser Ser Thr Ile
 215 220 225

cag tcc ccg aga gat gaa cag cgc cgt cgt ttg ccg ttg agc atc ggc 835
 Gln Ser Pro Arg Asp Glu Gln Arg Arg Arg Leu Pro Leu Ser Ile Gly
 230 235 240 245

gaa aac tgc aac ttt ggt gtc agc tcc gga atc tcc gga gtc att ctg 887
 Gln Asn Cys Asn Phe Gly Val Ser Ser Gly Ile Ile Gly Val Ser Leu
 250 255 260

gga cac aat tgc gac atc gga aat aac att gtc ttg gat gga gat acc 931
 Gly Asp Asn Cys Asp Ile Gly Asn Asn Ile Val Leu Asp Gly Asp Thr
 265 270 275

ctc att tgg ttc gca gcc gat gag gag tta cgc act atc gac tcc atc 979
 Pro Ile Trp Phe Ala Ala Asp Glu Glu Leu Arg Thr Ile Asp Ser Ile
 280 285 290

gaa ggc caa gca aat tgg tca atc aag cgt gaa tcc ggc ttc cat gag 1027
 Glu Gly Gln Ala Asn Trp Ser Ile Lys Arg Glu Ser Gly Phe His Glu
 295 300 305

cca att gcc cgc ctc aaa gct tgaccattt tcataaccag tgc 1071
 Pro Val Ala Arg Leu Lys Ala
 310 315

<210> 56

<211> 316

<212> PRT

<213> Corynebacterium glutamicum

<400> 56

Met Ser Glu Asn Ile Arg Gly Ala Gln Ala Val Gly Ile Ala Asn Ile
 1 5 10 15

Ala Met Asp Gly Thr Ile Leu Asp Thr Trp Tyr Pro Glu Pro Gln Ile
 20 25 30

Phe Asn Pro Asp Gln Trp Ala Glu Arg Tyr Pro Leu Glu Val Gly Thr

35

40

45

Thr Arg Leu Gly Ala Asn Glu Leu Thr Pro Arg Met Leu Gln Leu Val
 50 55 60
 Lys Leu Asp Gln Asp Arg Leu Val Glu Gln Val Ala Val Arg Thr Val
 65 70 75 80
 Ile Pro Asp Leu Ser Gln Pro Pro Val Asp Ala His Asp Val Tyr Leu
 85 90 95
 Arg Leu His Leu Leu Ser His Arg Leu Val Arg Pro His Glu Met His
 100 105 110
 Met Gln Asn Thr Leu Glu Leu Leu Ser Asp Val Val Trp Thr Asn Lys
 115 120 125
 Gly Pro Cys Leu Pro Glu Asn Phe Glu Trp Val Arg Gly Ala Leu Arg
 130 135 140
 Ser Arg Gly Leu Ile His Val Tyr Cys Val Asp Arg Leu Pro Arg Met
 145 150 155 160
 Val Asp Tyr Val Val Pro Pro Gly Val Arg Ile Ser Glu Ala Glu Arg
 165 170 175
 Val Arg Leu Gly Ala Tyr Leu Ala Pro Gly Thr Ser Val Leu Arg Glu
 180 185 190
 Gly Phe Val Ser Phe Asn Ser Gly Thr Leu Gly Ala Ala Lys Val Glu
 195 200 205
 Gly Arg Leu Ser Ser Gly Val Val Ile Gly Glu Gly Ser Glu Ile Gly
 210 215 220
 Leu Ser Ser Thr Ile Gln Ser Pro Arg Asp Glu Gln Arg Arg Arg Leu
 225 230 235 240
 Pro Leu Ser Ile Gly Gln Asn Cys Asn Phe Gly Val Ser Ser Gly Ile
 245 250 255
 Ile Gly Val Ser Leu Gly Asp Asn Cys Asp Ile Gly Asn Asn Ile Val
 260 265 270
 Leu Asp Gly Asp Thr Pro Ile Trp Phe Ala Ala Asp Glu Glu Leu Arg
 275 280 285
 Thr Ile Asp Ser Ile Glu Gly Gln Ala Asn Trp Ser Ile Lys Arg Glu
 290 295 300
 Ser Gly Phe His Glu Pro Val Ala Arg Leu Lys Ala
 305 310 315

<210> 57

<211> 1296

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1273)

<223> RNS02157

<400> 57

gggtggaatt ggcacgatgg tgcgcgcgga tgtttttgat cgggagaatt atcctgaagg 60

cacgggttttt agaaaaagacg acaagggatgg ggaactgtaa atg agc acg ctg gaa 115
Met Ser Thr Leu Glu
1 5

att tgg cca cag gtc att att aat acg tac ggc aac cca cca gtt gag 163
Thr Trp Pro Gln Val Ile Ile Asn Thr Tyr Gly Thr Pro Pro Val Glu
10 15 20

ctg gtg tcc ggc aag ggc gca acc gtc act aat gac cag ggc aat gtc 211
Leu Val Ser Gly Lys Gly Ala Thr Val Thr Asp Asp Gln Gly Asn Val
25 30 35

tac atc gac ttc ctc ggc ggc atc gca gtc aat ggc ttc ggc cag acc 254
Tyr Ile Asp Leu Leu Ala Gly Ile Ala Val Asn Ala Leu Gly His Ala
40 45 50

aat tgg ggc atc atc gag ggc gtc act aac aat atc ggc cca ctt ggt 307
His Pro Ala Ile Ile Glu Ala Val Thr Asn Gln Ile Gly Gln Leu Gly
55 60 65

cac gtc tcc aat ttc ttc gca tcc agg ccc ggc gtc aat ttc ggc gag 359
His Val Ser Asn Leu Phe Ala Ser Arg Pro Val Val Gln Val Ala Glu
70 75 80 85

gag ctc ctc aag cct ttt ttc gtc gtc gac ccc acc acc ctc ggc ggc cca 403
Gln Leu Ile Lys Arg Phe Ser Leu Asp Asp Ala Thr Leu Ala Ala Gln
90 95 100

acc cag gtt ttc ttc tgc aac ttc ggc ggc gaa gca aac gag gct gct 451
Thr Arg Val Phe Phe Cys Asn Ser Gly Ala Glu Ala Asn Gln Ala Ala
105 110 115

ctc aag att gca cgc ttg act ggt cgt tcc cag att ctc gct gca gtt 499
Phe Lys Ile Ala Arg Leu Thr Gly Arg Ser Arg Ile Leu Ala Ala Val
120 125 130

cac ggt ttc ccc ggc cgc acc atg ggt tcc ctc ggc ctg act ggc cag 547
His Gly Phe His Gly Arg Thr Met Gly Ser Leu Ala Leu Thr Gly Gln
135 140 145

cca gac aag cgt gaa ggc ttc ctg cca atg cca agc ggt gtg gag ttc 595
Pro Asp Lys Arg Glu Ala Phe Leu Pro Met Pro Ser Gly Val Glu Phe
150 155 160 165

tac cct tac ggc gac acc gat tac ttg cgc aaa atg gta gaa acc aac 643
Tyr Pro Tyr Gly Asp Thr Asp Tyr Leu Arg Lys Met Val Glu Thr Asn
170 175 180

cca aag gat gtg gct gct atc ttc ctc gag cca atc cag ggt gaa acc 691
Pro Thr Asp Val Ala Ala Ile Phe Leu Glu Pro Ile Gln Gly Glu Thr
185 190 195

ggc gtt gtt cca gca cct gaa gga ttc ctc aag gca gtg cgc gag ctg 739
Gly Val Val Pro Ala Pro Glu Gly Phe Leu Lys Ala Val Arg Glu Leu
200 205 210

tgc gat gag tac gcc atc ttg atg atc acc gat gaa atc cag act gcc 787
 Cys Asp Glu Tyr Gly Ile Leu Met Ile Thr Asp Glu Val Gln Thr Gly
 215 220 225

ggt gcc cgt acc gcc gat ttc ttt gca cat cag cac gat gcc gtt gtt 835
 Val Gly Arg Thr Gly Asp Phe Phe Ala His Gln His Asp Gly Val Val
 230 235 240 245

gcc gat gtc gag acc atg gcc aag gga ctt gcc gcc ggt ctt gcc atc 883
 Pro Asp Val Val Thr Met Ala Lys Gly Leu Gly Gly Gly Leu Pro Ile
 250 255 260

ggt gat tct ttc gcc act gcc cgt gca gct gaa ctg atg acc gca gcc 931
 Gly Ala Cys Leu Ala Thr Gly Arg Ala Ala Glu Leu Met Thr Pro Gly
 265 270 275

cag cac ggt acc act ttc cgt ggt gcc aac cca gtt gat tct gca act gcc 979
 Lys His Gly Thr Thr Phe Gly Gly Asn Pro Val Ala Cys Ala Ala Ala
 280 285 290

aag gca atg ctg tct gtt gtc gat gac gct ttc tgc gca gaa gtt gcc 1027
 Lys Ala Val Leu Ser Val Val Asp Asp Ala Phe Cys Ala Glu Val Ala
 295 300 305

gcc aag ggt gag ctg ttc aag gaa ctt ctt gcc aag gtt gat gcc gtt 1075
 Arg Lys Gly Glu Leu Phe Lys Glu Leu Leu Ala Lys Val Asp Gly Val
 310 315 320 325

gcc gac gtc cgt ggt aag gcc ttg atg ttg gcc gtc ctg ctg gcc gcc 1123
 Val Asp Val Arg Gly Arg Gly Leu Met Leu Gly Val Val Leu Glu Arg
 330 335 340

gcc gtc gca aag caa gct ctt ctt gat ggt ttt aag cac gcc att att 1171
 Asp Val Ala Lys Gln Ala Val Leu Asp Gly Phe Lys His Gly Val Ile
 345 350 355

ttg aat gca ccc gcc gac aac att atc cgt ttg acc ccg ccg ctg gtc 1219
 Leu Asn Ala Pro Ala Asp Asn Ile Ile Arg Leu Thr Pro Pro Leu Val
 360 365 370

atc acc gac gaa gaa atc gca gac gca gtc aag gct att gcc gag aca 1267
 Ile Thr Asp Glu Glu Ile Ala Asp Ala Val Lys Ala Ile Ala Glu Thr
 375 380 385

atc gca taaaggactc aaacttatga ctt 1296
 Ile Ala
 390

<110> 58

<111> 391

<112> PRT

<113> Corynebacterium glutamicum

<400> 58

Met Ser Thr Leu Glu Thr Trp Pro Gln Val Ile Ile Asn Thr Tyr Gly
 1 5 10 15

Thr Pro Pro Val Glu Leu Val Ser Gly Lys Gly Ala Thr Val Thr Asp
 20 25 30

Asp Gln Gly Asn Val Tyr Ile Asp Leu Leu Ala Gly Ile Ala Val Asn
 35 40 45
 Ala Leu Gly His Ala His Pro Ala Ile Ile Glu Ala Val Thr Asn Gln
 50 55 60
 Ile Gly Gln Leu Gly His Val Ser Asn Leu Phe Ala Ser Arg Pro Val
 65 70 75 80
 Val Glu Val Ala Glu Glu Leu Ile Lys Arg Phe Ser Leu Asp Asp Ala
 85 90 95
 Thr Leu Ala Ala Gln Thr Arg Val Phe Phe Cys Asn Ser Gly Ala Glu
 100 105 110
 Ala Asn Glu Ala Ala Phe Lys Ile Ala Arg Leu Thr Gly Arg Ser Arg
 115 120 125
 Ile Leu Ala Ala Val His Gly Phe His Gly Arg Thr Met Gly Ser Leu
 130 135 140
 Ala Leu Thr Gly Gln Pro Asp Lys Arg Glu Ala Phe Leu Pro Met Pro
 145 150 155 160
 Ser Gly Val Glu Phe Tyr Pro Tyr Gly Asp Thr Asp Tyr Leu Arg Lys
 165 170 175
 Met Val Glu Thr Asn Pro Thr Asp Val Ala Ala Ile Phe Leu Glu Pro
 180 185 190
 Ile Gln Gly Glu Thr Gly Val Val Pro Ala Pro Glu Gly Phe Leu Lys
 195 200 205
 Ala Val Arg Glu Leu Cys Asp Glu Tyr Gly Ile Leu Met Ile Thr Asp
 210 215 220
 Glu Val Gln Thr Gly Val Gly Arg Thr Gly Asp Phe Phe Ala His Gln
 225 230 235 240
 His Asp Gly Val Val Pro Asp Val Val Thr Met Ala Lys Gly Leu Gly
 245 250 255
 Gly Gly Leu Pro Ile Gly Ala Cys Leu Ala Thr Gly Arg Ala Ala Glu
 260 265 270
 Leu Met Thr Pro Gly Lys His Gly Thr Thr Phe Gly Gly Asn Pro Val
 275 280 285
 Ala Cys Ala Ala Ala Lys Ala Val Leu Ser Val Val Asp Asp Ala Phe
 290 295 300
 Cys Ala Glu Val Ala Arg Lys Gly Glu Leu Phe Lys Glu Leu Leu Ala
 305 310 315 320
 Lys Val Asp Gly Val Val Asp Val Arg Gly Arg Gly Leu Met Leu Gly
 325 330 335
 Val Val Leu Glu Arg Asp Val Ala Lys Gln Ala Val Leu Asp Gly Phe
 340 345 350

Lys His Gly Val Ile Leu Asn Ala Pro Ala Asp Asn Ile Ile Arg Leu
355 360 365

Thr Pro Pro Leu Val Ile Thr Asp Glu Glu Ile Ala Asp Ala Val Lys
370 375 380

Ala Ile Ala Glu Thr Ile Ala
385 390

<210> 59

<211> 1008

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(985)

<223> K00307.1

<400> 59

agggagaggt tatcgatatt ggagcgcaaa agatttggc gaacacgtgc ggtacctaac 60

agaaatagt agaatccaa agactgcgc aaggaatc atg agt aat gtt gca 115
Met Ser Asn Thr Ala
1 5

ggc ccc cgc ggg agt tcc cat cag gca gat gtc tag tcc aat caa aag 163
Gly Pro Arg Gly Arg Ser His Gln Ala Asp Ala Ala Pro Asn Gln Lys
10 15 20

gca cag aat ttc gga cca tcc gcc aac agg ctt ttc gga att cta ggc 211
Ala Gln Asn Phe Gly Pro Ser Ala Lys Arg Leu Phe Gly Ile Leu Gly
25 30 35

cat gac cgt aac acc tta att ttc gtt atc ttc cta gcc gtc ctg agc 259
His Asp Arg Asn Thr Leu Ile Phe Val Ile Phe Leu Ala Val Leu Ser
40 45 50

gtt gga ctt acc gtc ttg ggc cca tgg ttg ctg ggt aaa gcc acc aac 307
Val Gly Leu Thr Val Leu Gly Pro Trp Leu Leu Gly Lys Ala Thr Asn
55 60 65

gtg gtg ttt gaa gga ttc cta tcc aag cgc atg ccg gct ggt ggc tca 355
Val Val Phe Glu Gly Phe Leu Ser Lys Arg Met Pro Ala Gly Ala Ser
70 75 80 85

aag gaa gat atc atc gcg cag ttg cag gct gca ggt aaa cat aat cag 403
Lys Glu Asp Ile Ile Ala Gln Leu Gln Ala Ala Gly Lys His Asn Gln
90 95 100

gct tcc atg atg gaa gac atg aac ctt gtt cca gcc tca gcc att gat 451
Ala Ser Met Met Glu Asp Met Asn Leu Val Pro Gly Ser Gly Ile Asp
105 110 115

ttt gaa aaa tta gcc atg atc ctc gga ctg gtg atc ggt gct tat ctc 499
Phe Glu Lys Leu Ala Met Ile Leu Gly Leu Val Ile Gly Ala Tyr Leu
120 125 130

atc ggt agc atg ttg tcc ttg ttc cag gcc cgg atg ctc aac cgc atc 547
Ile Gly Ser Leu Leu Ser Leu Phe Gln Ala Arg Met Leu Asn Arg Ile

135	140	145	
gtg caa agt gcc atg cac cgg ctg cgc atg gag gtg gag gaa aaa atc			595
Val Gln Ser Ala Met His Arg Leu Arg Met Glu Val Glu Glu Lys Ile			
150	155	160	165
cac cgc cta cgg ctg agc tat ttc gat tcc atc aaa cgt ggt gat ctg			643
His Arg Leu Pro Leu Ser Tyr Phe Asp Ser Ile Lys Arg Gly Asp Leu			
	170	175	180
ctt agc cgt gtg acc aac gat gtg gat aat atc ggt caa tcc ctg caa			691
Leu Ser Arg Val Thr Asn Asp Val Asp Asn Ile Gly Gln Ser Leu Gln			
	185	190	195
caa acc atg tca cag gag atc aat tcc cta ctg acc gtc atc ggt gtg			739
Gln Thr Leu Ser Gln Ala Ile Thr Ser Leu Leu Thr Val Ile Gly Val			
	200	205	210
ttg gtg atg atg ctt atc atc tcc cca ctg ctg gca cta gtg gag ctg			787
Leu Val Met Met Phe Ile Ile Ser Pro Leu Leu Ala Leu Val Ala Leu			
	215	220	225
gta tcc att cgg gtc acc atc gtg gtc act gtg gtg gtt gag agc cgt			835
Val Ser Ile Pro Val Thr Ile Val Val Thr Val Val Val Ala Ser Arg			
	230	235	240
tcc cag aaa ctc ttt cgg gaa cag tgg aac tgg acc gtt att ttg aat			883
Ser Gln Lys Leu Phe Ala Gln Gln Trp Lys Gln Thr Gly Ile Leu Asn			
	250	255	260
gag cgc ctg gag gaa acc tac tct ggc cac gcc gtg gtt aag gtt ttc			931
Ala Arg Leu Glu Glu Thr Tyr Ser Gly His Ala Val Val Lys Val Phe			
	265	270	275
gga cac caa aag gat gtt caa gaa gca ttc gac gaa gaa aat caa got			979
Gly His Gln Lys Asp Val Gln Glu Ala Phe Glu Glu Glu Asn Gln Ala			
	280	285	290
tgt gta caaggccagc ttgggtgccc agt			1008
Cys Val			
	295		

<210> 60

<211> 298

<212> PRT

<213> Corynebacterium glutamicum

<400> 60

Met	Ser	Asn	Thr	Ala	Gly	Pro	Arg	Gly	Arg	Ser	His	Gln	Ala	Asp	Ala
1				5					10					15	

Ala	Pro	Asn	Gln	Lys	Ala	Gln	Asn	Phe	Gly	Pro	Ser	Ala	Lys	Arg	Leu
			20					25					30		

Phe	Gly	Ile	Leu	Gly	His	Asp	Arg	Asn	Thr	Leu	Ile	Phe	Val	Ile	Phe
		35						40				45			

Leu	Ala	Val	Leu	Ser	Val	Gly	Leu	Thr	Val	Leu	Gly	Pro	Trp	Leu	Leu
		50				55					60				

Gly Lys Ala Thr Asn Val Val Phe Glu Gly Phe Leu Ser Lys Arg Met
65 70 75 80

Pro Ala Gly Ala Ser Lys Glu Asp Ile Ile Ala Gln Leu Gln Ala Ala
85 90 95

Gly Lys His Asn Gln Ala Ser Met Met Glu Asp Met Asn Leu Val Pro
100 105 110

Gly Ser Gly Ile Asp Phe Glu Lys Leu Ala Met Ile Leu Gly Leu Val
115 120 125

Ile Gly Ala Tyr Leu Ile Gly Ser Leu Leu Ser Leu Phe Gln Ala Arg
130 135 140

Met Leu Asn Arg Ile Val Gln Ser Ala Met His Arg Leu Arg Met Glu
145 150 155 160

Val Glu Glu Lys Ile His Arg Leu Pro Leu Ser Tyr Phe Asp Ser Ile
165 170 175

Lys Arg Gly Asp Leu Leu Ser Arg Val Thr Asn Asp Val Asp Asn Ile
180 185 190

Gly Gln Ser Leu Gln Gln Thr Leu Ser Gln Ala Ile Thr Ser Leu Leu
195 200 205

Thr Val Ile Gly Val Leu Val Met Met Phe Ile Ile Ser Pro Leu Leu
210 215 220

Ala Leu Val Ala Leu Val Ser Ile Pro Val Thr Ile Val Val Thr Val
225 230 235 240

Val Val Ala Ser Arg Ser Gln Lys Leu Phe Ala Glu Gln Trp Lys Gln
245 250 255

Thr Gly Ile Leu Asn Ala Arg Leu Glu Glu Thr Tyr Ser Gly His Ala
260 265 270

Val Val Lys Val Phe Gly His Gln Lys Asp Val Gln Glu Ala Phe Glu
275 280 285

Glu Glu Asn Gln Ala Cys Val
290 295

<210> 61

<211> 426

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(426)

<223> RXC00861

<400> 61

atg gct cct cac aag gtc atg ctg att acc act ggt act cag ggt gag 48
Met Ala Pro His Lys Val Met Leu Ile Thr Thr Gly Thr Gln Gly Glu
1 5 10 15

cct atg gct gag ctg tct cgg atg gag cgt cgt gag cac cga cag atc 95
 Pro Met Ala Ala Leu Ser Arg Met Ala Arg Arg Glu His Arg Gln Ile
 20 25 30

act gtc cgt gat gga gac ttg att atc ctt tct tcc tcc ctg gtt cca 144
 Thr Val Arg Asp Gly Asp Leu Ile Ile Leu Ser Ser Ser Leu Val Pro
 35 40 45

ggt aac gaa gaa gca gtg ttc ggt gtc atc aac atg ctg gct cag atc 192
 Gly Asn Glu Glu Ala Val Phe Gly Val Ile Asn Met Leu Ala Gln Ile
 50 55 60

ggt aca act gtt gtt acc ggt cgc gac ggc aag gtc cac aac tgg ggc 240
 Gly Ala Thr Val Val Thr Gly Arg Asp Ala Lys Val His Thr Ser Gly
 65 70 75 80

cct cgt tct tct gaa gag ctg tgg ttc tgg tac aac gct gtt cgt cgt 288
 His Gly Tyr Ser Gly Glu Leu Leu Phe Leu Tyr Asn Ala Ala Arg Pro
 85 90 95

aac aac gct atg cct gtc cac cgc gag tgg cgc cac ctg cgc gcc aac 336
 Lys Asn Ala Met Pro Val His Gly Glu Trp Arg His Leu Arg Ala Asn
 100 105 110

aac gaa ctg act atc tcc act ggt gtt aac cgc gac aac gtt gtt ctt 384
 Lys Glu Leu Ala Ile Ser Thr Gly Val Asn Arg Asp Asn Val Val Leu
 115 120 125

gtc aa aac agt gtt ggt ggt gtt atg gtc aac gtt tgg gaa 432
 Ala Gln Asn Gly Val Val Val Asp Met Val Asn Gly Arg Ala
 130 135 140

<210> 62
 <211> 142
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 62
 Met Ala Pro His Lys Val Met Leu Ile Thr Thr Gly Thr Gln Gly Glu
 1 5 10 15

Pro Met Ala Ala Leu Ser Arg Met Ala Arg Arg Glu His Arg Gln Ile
 20 25 30

Thr Val Arg Asp Gly Asp Leu Ile Ile Leu Ser Ser Ser Leu Val Pro
 35 40 45

Gly Asn Glu Glu Ala Val Phe Gly Val Ile Asn Met Leu Ala Gln Ile
 50 55 60

Gly Ala Thr Val Val Thr Gly Arg Asp Ala Lys Val His Thr Ser Gly
 65 70 75 80

His Gly Tyr Ser Gly Glu Leu Leu Phe Leu Tyr Asn Ala Ala Arg Pro
 85 90 95

Lys Asn Ala Met Pro Val His Gly Glu Trp Arg His Leu Arg Ala Asn
 100 105 110

Lys Glu Leu Ala Ile Ser Thr Gly Val Asn Arg Asp Asn Val Val Leu

115

120

125

Ala Gln Asn Gly Val Val Val Asp Met Val Asn Gly Arg Ala
 130 135 140

<210> 63
 <211> 1066
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1066)
 <223> R0000866

<400> 63
 gntcgaacgt agagatcat agacttcaa atatggtcc aatgacag gacttgagg 60

ctctcgaat atacatgaaa aaagctggag tctataaat atg aat gat tcc cga 115
 Met Asn Asp Ser Arg
 1 5

aat cgt ggc tgg aag gtt acc cgt aag ggc cgc cca cca gaa gct gct 163
 Asn Arg Gly Arg Lys Val Thr Arg Lys Ala Gly Pro Pro Gln Ala Gly
 10 15 20

cag gaa aac cat ctg gat acc cca gtc ttt cag gaa cca gat gct tcc 211
 Gln Glu Asn His Leu Asp Thr Pro Val Phe Gln Ala Pro Asp Ala Ser
 25 30 35

tct aac cag acc gct gta aaa gct gag acc ggc gga aac gaa aat cgg 259
 Ser Asn Gln Ser Ala Val Lys Ala Glu Thr Ala Gly Asn Asp Asn Arg
 40 45 50

gat gct ggc caa ggt gct caa gga tcc caa gat tct cag ggt tcc cag 307
 Asp Ala Ala Gln Gly Ala Gln Gly Ser Gln Asp Ser Gln Gly Ser Gln
 55 60 65

aac gct caa ggt tcc cag aac cgc gag tcc gga aac aac aac cgc aac 355
 Asn Ala Gln Gly Ser Gln Asn Arg Glu Ser Gly Asn Asn Asn Arg Asn
 70 75 80 85

cgt tcc aac aac aac cgt cgc ggt ggt cgt gga cgt cgt gga tcc gga 403
 Arg Ser Asn Asn Asn Arg Arg Gly Gly Arg Gly Arg Arg Gly Ser Gly
 90 95 100

aac gcc aat gag ggc gcg aac aac aac agc ggt aac cag aac cgt cag 451
 Asn Ala Asn Glu Gly Ala Asn Asn Asn Ser Gly Asn Gln Asn Arg Gln
 105 110 115

ggc gga aac cgt ggc aac cgc ggt ggc gga cgc cga aac gtt gtt aag 499
 Gly Gly Asn Arg Gly Asn Arg Gly Gly Gly Arg Arg Asn Val Val Lys
 120 125 130

tcg atg cag ggt ggc gat ctg acc cag cgc ctg cca gag cca cca aag 547
 Ser Met Gln Gly Ala Asp Leu Thr Gln Arg Leu Pro Glu Pro Pro Lys
 135 140 145

gca cgc cca aac ggt ctg cgt att tac gca ctt ggt ggc att tcc gaa 595
 Ala Pro Ala Asn Gly Leu Arg Ile Tyr Ala Leu Gly Gly Ile Ser Glu

150	155	160	165	
atc ggt cgc aac atg acc gtg ttt gag tac aac aac cgt ctg etc atc				643
Ile Gly Arg Asn Met Thr Val Phe Glu Tyr Asn Asn Arg Leu Leu Ile	170	175	180	
gtg gac tgt ggt gtg etc ttc cca tct tca ggt gag cca ggc gtt gac				691
Val Asp Cys Gly Val Leu Phe Pro Ser Ser Gly Glu Pro Gly Val Asp	185	190	195	
ctg att ctt cct gac ttc ggc cca att gag gat cac ctg cac cgc gtc				739
Leu Ile Leu Pro Asp Phe Gly Pro Ile Glu Asp His Leu His Arg Val	200	205	210	
gat gca tgg gtg gtt act cac gga cac gaa gac cac att ggt gat att				787
Asp Ala Leu Val Val Thr His Gly His Glu Asp His Ile Gly Ala Ile	215	220	225	
cca tga tta tta aac ctg cgc aac gat atc cca att tta gaa tta cgt				835
Pro Trp Leu Leu Lys Leu Arg Asn Asp Ile Pro Ile Leu Ala Ser Arg	230	235	240	245
tta cca tgg gct ctg att gga gct aag tgt aag gaa cac cgt cag ctt				883
Phe Thr Leu Ala Leu Ile Ala Ala Lys Cys Lys Glu His Arg Gln Arg	250	255	260	
cag cag tta atg gag gtt aac gag cag tta gat gaa gaa cgt gga cgt				931
Pro Lys Leu Ile Glu Val Asn Glu Gln Ser Asn Glu Asp Arg Gly Pro	265	270	275	
tta cac att cgt tta tgg gct gtt aac cac tta atc cca gaa tga ctt				979
Phe Asn Ile Arg Phe Trp Ala Val Asn His Ser Ile Pro Asp Cys Leu	280	285	290	
ggt ttt gct atc aag act cct gct ggt ttg gtc atc cac acc ggt gac				1027
Gly Leu Ala Ile Lys Thr Pro Ala Gly Leu Val Ile His Thr Gly Asp	295	300	305	
atc aag ctg gat cag act cct cct gat gga cgc cca act				1066
Ile Lys Leu Asp Gln Thr Pro Pro Asp Gly Arg Pro Thr	310	315	320	

<210> 64

<211> 322

<212> PRT

<213> Corynebacterium glutamicum

<400> 64

Met	Asn	Asp	Ser	Arg	Asn	Arg	Gly	Arg	Lys	Val	Thr	Arg	Lys	Ala	Gly
1					5				10					15	

Pro	Pro	Glu	Ala	Gly	Gln	Glu	Asn	His	Leu	Asp	Thr	Pro	Val	Phe	Gln
		20						25					30		

Ala	Pro	Asp	Ala	Ser	Ser	Asn	Gln	Ser	Ala	Val	Lys	Ala	Glu	Thr	Ala
		35					40					45			

Gly	Asn	Asp	Asn	Arg	Asp	Ala	Ala	Gln	Gly	Ala	Gln	Gly	Ser	Gln	Asp
	50					55				60					

Ser Gln Gly Ser Gln Asn Ala Gln Gly Ser Gln Asn Arg Glu Ser Gly
 65 70 75 80
 Asn Asn Asn Arg Asn Arg Ser Asn Asn Asn Arg Arg Gly Gly Arg Gly
 85 90 95
 Arg Arg Gly Ser Gly Asn Ala Asn Glu Gly Ala Asn Asn Asn Ser Gly
 100 105 110
 Asn Gln Asn Arg Gln Gly Gly Asn Arg Gly Asn Arg Gly Gly Gly Arg
 115 120 125
 Arg Asn Val Val Lys Ser Met Gln Gly Ala Asp Leu Thr Gln Arg Leu
 130 135 140
 Pro Glu Pro Pro Lys Ala Pro Ala Asn Gly Leu Arg Ile Tyr Ala Leu
 145 150 155 160
 Gly Gly Ile Ser Glu Ile Gly Arg Asn Met Thr Val Phe Glu Tyr Asn
 165 170 175
 Asn Arg Leu Leu Ile Val Asp Cys Gly Val Leu Phe Pro Ser Ser Gly
 180 185 190
 Glu Pro Gly Val Asp Leu Ile Leu Pro Asp Phe Gly Pro Ile Glu Asp
 195 200 205
 His Leu His Arg Val Asp Ala Leu Val Val Thr His Gly His Glu Asp
 210 215 220
 His Ile Gly Ala Ile Pro Trp Leu Leu Lys Leu Arg Asn Asp Ile Pro
 225 230 235 240
 Ile Leu Ala Ser Arg Phe Thr Leu Ala Leu Ile Ala Ala Lys Gys Lys
 245 250 255
 Glu His Arg Gln Arg Pro Lys Leu Ile Glu Val Asn Glu Gln Ser Asn
 260 265 270
 Glu Asp Arg Gly Pro Phe Asn Ile Arg Phe Trp Ala Val Asn His Ser
 275 280 285
 Ile Pro Asp Cys Leu Gly Leu Ala Ile Lys Thr Pro Ala Gly Leu Val
 290 295 300
 Ile His Thr Gly Asp Ile Lys Leu Asp Gln Thr Pro Pro Asp Gly Arg
 305 310 315 320
 Pro Thr

<210> 65
 <211> 1527
 <212> DNA
 <213> Corynebacterium glutamicum

 <220>
 <221> CDS
 <222> (101)..(1504)
 <223> RXC02095

Pho	Ala	Ser	Thr	Trp	Ser	Ala	Gln	Gln	Lys	Ala	Ala	Asp	Leu	Thr	Thr		
215						220					225						
cat	gtg	gaa	gaa	act	gtc	acg	ggg	atc	ggc	gtg	gtc	aag	gca	ttt	gcg	835	
His	Val	Glu	Glu	Thr	Val	Thr	Gly	Ile	Arg	Val	Val	Lys	Ala	Phe	Ala		
230					235				240					245			
cag	gaa	gac	ggc	gag	acc	gac	aaa	tty	gat	ctc	acc	gca	cgt	gag	tta	883	
Gln	Glu	Asp	Arg	Glu	Thr	Asp	Lys	Leu	Asp	Leu	Thr	Ala	Arg	Glu	Leu		
				250				255						260			
ttt	goc	cag	ggc	atg	ggc	act	gca	cgt	ctg	acg	gca	aag	ttc	atc	ccc	931	
Phe	Ala	Gln	Arg	Met	Arg	Thr	Ala	Arg	Leu	Thr	Ala	Lys	Phe	Ile	Pro		
				265				270					275				
atg	gtt	gag	cag	ctt	cag	cag	ctt	gct	tig	gig	gtc	aac	att	gtt	ggc	979	
Met	Val	Glu	Gln	Leu	Pro	Gln	Leu	Ala	Leu	Val	Val	Asn	Ile	Val	Gly		
				280			285					290					
agg	ggg	tat	tig	gac	atg	act	ggg	cac	atc	arg	gig	ggc	acc	ttt	gtg	1027	
Gly	Gly	Tyr	Leu	Ala	Met	Thr	Gly	His	Ile	Thr	Val	Gly	Thr	Phe	Val		
	295						300					305					
ggg	tat	tat	tac	tat	ctc	act	agg	tig	gag	ggg	ggg	gct	agg	tcc	ctg	1075	
Ala	Phe	Ser	Ser	Tyr	Leu	Thr	Ser	Leu	Ser	Ala	Val	Ala	Arg	Ser	Leu		
	310					315				320					325		
ggg	ggg	atg	ctc	atg	agg	atg	cag	tig	ggg	ctg	ttt	ttt	ctc	gag	ggc	1123	
Ser	Gly	Met	Leu	Met	Arg	Val	Gln	Leu	Ala	Leu	Ser	Ser	Val	Glu	Arg		
				330				335						340			
atc	ttt	gaa	gtc	att	gat	ctt	cag	ctt	gaa	ggc	acc	gat	ctt	gca	cac	1171	
Ile	Phe	Glu	Val	Ile	Asp	Leu	Gln	Pro	Glu	Arg	Thr	Asp	Pro	Ala	His		
				345				350					355				
ccc	ctg	tca	ctt	ccc	gac	act	ccc	ctg	ggg	ctg	tcc	ttc	aac	gac	gta	1219	
Pro	Leu	Ser	Leu	Pro	Asp	Thr	Pro	Leu	Gly	Leu	Ser	Phe	Asn	Asn	Val		
				360				365				370					
gat	ttc	cgt	ggg	att	ctc	aac	ggg	ttt	gag	ctg	ggg	gtt	cag	goc	ggg	1267	
Asp	Phe	Arg	Gly	Ile	Leu	Asn	Gly	Phe	Glu	Leu	Gly	Val	Gln	Ala	Gly		
				375			380				385						
gaa	acc	gtt	gtg	tig	gtg	ggc	ccc	cca	ggg	tca	ggc	aag	acc	atg	gct	1315	
Glu	Thr	Val	Val	Leu	Val	Gly	Pro	Pro	Gly	Ser	Gly	Lys	Thr	Met	Ala		
				390			395			400				405			
gtg	cag	ctt	gct	gga	aac	ttt	tat	caa	cca	gac	agg	ggc	cac	atc	gcc	1363	
Val	Gln	Leu	Ala	Gly	Asn	Phe	Tyr	Gln	Pro	Asp	Ser	Gly	His	Ile	Ala		
				410				415						420			
ttt	gat	agg	aac	ggc	cat	ggc	act	ggc	ttc	gac	gac	ctc	acc	cac	agg	1411	
Phe	Asp	Ser	Asn	Gly	His	Arg	Thr	Arg	Phe	Asp	Asp	Leu	Thr	His	Ser		
				425				430					435				
gat	atc	ggc	agg	aat	ctc	atc	ggg	ggt	ttt	gat	gag	ccg	ttc	tig	tac	1459	
Asp	Ile	Arg	Arg	Asn	Leu	Ile	Ala	Val	Phe	Asp	Glu	Pro	Phe	Leu	Tyr		
				440			445					450					
tcc	tcc	tcc	ata	ccg	cga	gaa	cat	ctc	gat	ggg	ttt	gga	tgt	cag		1504	
Ser	Ser	Ser	Ile	Pro	Arg	Glu	His	Leu	Asp	Gly	Phe	Gly	Cys	Gln			

455

460

465

tgatgagcag atcgaacacg cag

1527

<210> 66

<211> 468

<212> PRT

<213> Corynebacterium glutamicum

<400> 66

Met Lys Thr Glu Gln Ser Gln Lys Ala Gln Leu Ala Pro Lys Lys Ala
 1 5 10 15

Pro Glu Lys Pro Gln Arg Ile Arg Gln Leu Ile Ser Val Ala Trp Gln
 20 25 30

Arg Pro Trp Leu Thr Ser Phe Thr Val Ile Ser Ala Leu Ala Ala Thr
 35 40 45

Leu Phe Glu Leu Thr Leu Pro Leu Leu Thr Gly Gly Ala Ile Asp Ile
 50 55 60

Ala Leu Gly Asn Thr Gly Asp Thr Leu Thr Thr Asp Leu Leu Asp Arg
 65 70 75 80

Ile Thr Pro Ser Gly Leu Ser Val Leu Thr Ser Val Ile Ala Leu Ile
 85 90 95

Val Leu Leu Ala Leu Leu Arg Tyr Ala Ser Gln Phe Gly Arg Arg Tyr
 100 105 110

Thr Ala Gly Lys Leu Ser Met Gly Val Gln His Asp Val Arg Leu Lys
 115 120 125

Thr Met Arg Ser Leu Gln Asn Leu Asp Gly Pro Gly Gln Asp Ser Ile
 130 135 140

Arg Thr Gly Gln Val Val Ser Arg Ser Ile Ser Asp Ile Asn Met Val
 145 150 155 160

Gln Ser Leu Val Ala Met Leu Pro Met Leu Ile Gly Asn Val Val Lys
 165 170 175

Leu Val Leu Thr Leu Val Ile Met Leu Ala Ile Ser Pro Pro Leu Thr
 180 185 190

Ile Ile Ala Ala Val Leu Val Pro Leu Leu Leu Trp Ala Val Ala Tyr
 195 200 205

Ser Arg Lys Ala Leu Phe Ala Ser Thr Trp Ser Ala Gln Gln Lys Ala
 210 215 220

Ala Asp Leu Thr Thr His Val Glu Glu Thr Val Thr Gly Ile Arg Val
 225 230 235 240

Val Lys Ala Phe Ala Gln Glu Asp Arg Glu Thr Asp Lys Leu Asp Leu
 245 250 255

Thr Ala Arg Glu Leu Phe Ala Gln Arg Met Arg Thr Ala Arg Leu Thr
 260 265 270

Ala Lys Phe Ile Pro Met Val Glu Gln Leu Pro Gln Leu Ala Leu Val
 275 280 285

Val Asn Ile Val Gly Gly Gly Tyr Leu Ala Met Thr Gly His Ile Thr
 290 295 300

Val Gly Thr Phe Val Ala Phe Ser Ser Tyr Leu Thr Ser Leu Ser Ala
 305 310 315 320

Val Ala Arg Ser Leu Ser Gly Met Leu Met Arg Val Gln Leu Ala Leu
 325 330 335

Ser Ser Val Glu Arg Ile Phe Glu Val Ile Asp Leu Gln Pro Glu Arg
 340 345 350

Thr Asp Pro Ala His Pro Leu Ser Leu Pro Asp Thr Pro Leu Gly Leu
 355 360 365

Ser Phe Asn Asn Val Asp Phe Arg Gly Ile Leu Asn Gly Phe Glu Leu
 370 375 380

Gly Val Gln Ala Gly Glu Thr Val Val Leu Val Gly Pro Pro Gly Ser
 385 390 395 400

Gly Lys Thr Met Ala Val Gln Leu Ala Gly Asn Phe Tyr Gln Pro Asp
 405 410 415

Ser Gly His Ile Ala Phe Asp Ser Asn Gly His Arg Thr Arg Phe Asp
 420 425 430

Asp Leu Thr His Ser Asp Ile Arg Arg Asn Leu Ile Ala Val Phe Asp
 435 440 445

Gln Pro Phe Leu Tyr Ser Ser Ser Ile Pro Arg Glu His Leu Asp Gly
 450 455 460

Phe Gly Cys Gln
 465

<210> 67
 <211> 295
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (84)..(272)
 <223> RXC03185

<400> 67
 agcgcccaac cggttcagacc agcgggtttct ctgaggatgc aaagtcacatg atgggtnagg 60
 tcaactgagct gtccgaaacc acc atg aat gat ctt gca gct gaa ggt gaa aac 113
 Met Asn Asp Leu Ala Ala Glu Gly Glu Asn
 1 5 10
 gat cct tac cgc atg gtt cag cag ctg cgc cgc aag ctg tat cgc ttc 161
 Asp Pro Tyr Arg Met Val Gln Gln Leu Arg Arg Lys Leu Ser Arg Phe
 15 20 25

gtc gag cag aag tgg aag cgc cag ccg gtc atc atg cca acc gtc att 209
Val Glu Gln Lys Trp Lys Arg Gln Pro Val Ile Met Pro Thr Val Ile
30 35 40

cgc atg act gcg gaa acc acg cac atc ggt gac gat gag gtt cgc gct 257
Pro Met Thr Ala Glu Thr Thr His Ile Gly Asp Asp Glu Val Arg Ala
45 50 55

tca cgc gag tcc ctg taaaagcatt togtttttcg acg 295
Ser Arg Glu Ser Leu
60

<210> 68

<211> 63

<212> PRT

<213> Corynebacterium glutamicum

<220> 68

Met Asn Asp Leu Ala Ala Glu Gly Glu Asn Asp Pro Tyr Arg Met Val
1 5 10 15

Gln Gln Leu Arg Arg Lys Leu Ser Arg Phe Val Glu Gln Lys Trp Lys
20 25 30

Arg Gln Pro Val Ile Met Pro Thr Val Ile Pro Met Thr Ala Glu Thr
35 40 45

Thr His Ile Gly Asp Asp Glu Val Arg Ala Ser Arg Glu Ser Leu
50 55 60

<210> 69

<211> 1170

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1147)

<223> RXA00115

<400> 69

tggattctcg agtctgtaca cccttgatca aagcccgagt gtcccgtaga ttaactttgt 60

cgtatattgt gacctacacc ccatactggt aggagttttc atg ctc gac aat agt 115
Met Leu Asp Asn Ser
1 5

ttt tac acc gca gag gtt cag gcc cca tac gaa acc gct tcc att ggc 163
Phe Tyr Thr Ala Glu Val Gln Gly Pro Tyr Glu Thr Ala Ser Ile Gly
10 15 20

cgg ctc gaa ctc gaa gaa ggg ggt ctg att gag gat tgc tgg ttg gct 211
Arg Leu Glu Leu Glu Glu Gly Gly Val Ile Glu Asp Cys Trp Leu Ala
25 30 35

tac gct aca gct gga acg ctc aac gag gac aag tcc aac gcc atc ctc 259
Tyr Ala Thr Ala Gly Thr Leu Asn Glu Asp Lys Ser Asn Ala Ile Leu
40 45 50

att ccg aag tgg tac tcc gga acc cat cag acc tgg ttc cag cag tac	307
Ile Pro Thr Trp Tyr Ser Gly Thr His Gln Thr Trp Phe Gln Gln Tyr	
55 60 65	
atc ggc aat gat cat gcg ctg gat cca tca aag tat ttc atc atc tcc	355
Ile Gly Thr Asp His Ala Leu Asp Pro Ser Lys Tyr Phe Ile Ile Ser	
70 75 80 85	
atc aac caa atc ggt aat ggt ttg tgg gtc tcc cct gcc aac aag gct	403
Ile Asn Gln Ile Gly Asn Gly Leu Ser Val Ser Pro Ala Asn Thr Ala	
90 95 100	
gat gac agc atc tgg aag tcc aag ttc ccg aat gtt cgc att ggt gat	451
Asp Asp Ser Ile Ser Met Ser Lys Phe Pro Asn Val Arg Ile Gly Asp	
105 110 115	
gat gtc gtt gcc cag gcc agg ctc ttg cgt caa gag ttt cgt att acc	499
Asp Val Val Ala Gln Asp Arg Leu Leu Arg Gln Gln Phe Gly Ile Thr	
120 125 130	
gag ttc ttt gcc gtr gtt gat gtt tgg atg ggt gcc cag caa acc tat	547
Gln Leu Phe Ala Val Val Gly Gly Ser Met Gly Ala Gln Gln Thr Tyr	
135 140 145	
gag tgg att gtt cgc ttc cct gcc caa gtt cat cga gcc gct ccg atc	595
Gln Trp Ile Val Arg Phe Pro Asp Gln Val His Arg Ala Ala Pro Ile	
150 155 160 165	
ggc ggc aat ggc aag aac act ctt cat gat ttc atc ttc acc cag act	643
Ala Gly Thr Ala Lys Asn Thr Pro His Asp Phe Ile Phe Thr Gln Thr	
170 175 180	
ctt aat gag acc gtt gag gcc gat caa ggg ttc aat ggc gcc gaa tac	691
Ile Asn Gln Thr Val Glu Ala Asp Pro Gly Phe Asn Gly Gly Gln Tyr	
185 190 195	
tcc tcc cat gaa gag gta gat gat gga ctt cgc cgt caa tgg cat ctt	739
Ser Ser His Glu Glu Val Ala Asp Gly Leu Arg Arg Gln Ser His Leu	
200 205 210	
tgg gct gcc atg gga ttt tcc aca gag ttc tgg aag cag gag gca tgg	787
Trp Ala Ala Met Gly Phe Ser Thr Glu Phe Trp Lys Gln Glu Ala Trp	
215 220 225	
cgt cgc ctg gga ctt gaa agt aag gag tca gtg ctc gcg gac ttc ctg	835
Arg Arg Leu Gly Leu Glu Ser Lys Glu Ser Val Leu Ala Asp Phe Leu	
230 235 240 245	
gat ccg ctg ttc atg tcc atg gat cct aat acc ttg ctc aac aac gct	883
Asp Pro Leu Phe Met Ser Met Asp Pro Asn Thr Leu Leu Asn Asn Ala	
250 255 260	
tgg aag tgg cag cat gcc gat gtc tct cgc cac acc gcc gcc gac ttg	931
Trp Lys Trp Gln His Gly Asp Val Ser Arg His Thr Gly Gly Asp Leu	
265 270 275	
gca gcc gat ctt gcc cga gtc aag gct aag acc ttc gtt atg ccc atc	979
Ala Ala Ala Leu Gly Arg Val Lys Ala Lys Thr Phe Val Met Pro Ile	
280 285 290	

agc gag gac atg ttc ttt cct gtt cgt gac tgt gcc gca gaa caa gca 1027
 Ser Glu Asp Met Phe Phe Pro Val Arg Asp Cys Ala Ala Glu Gln Ala
 295 300 305
 ctc atc cca gcc agc gag ctt cga gtg atc gaa gac atc gcc ggt cac 1075
 Leu Ile Pro Gly Ser Glu Leu Arg Val Ile Glu Asp Ile Ala Gly His
 310 315 320 325
 ctt ggg ctt ttt aac gtc tct gag aat tac atc cca cag atc gac aaa 1123
 Leu Gly Leu Phe Asn Val Ser Glu Asn Tyr Ile Pro Gln Ile Asp Lys
 330 335 340
 aat ctg aaa gag ctg ttc gag agc taacacactga tgcacaaagag cct 1170
 Asn Leu Lys Glu Leu Phe Glu Ser
 345

<210> 30

<211> 349

<212> PRT

<213> Corynebacterium glutamicum

<400> 30

Met Leu Asp Asn Ser Phe Tyr Thr Ala Glu Val Gln Gly Pro Tyr Glu
 1 5 10 15
 Thr Ala Ser Ile Gly Arg Leu Glu Leu Glu Gly Gly Val Ile Glu
 20 25 30
 Asp Cys Trp Leu Ala Tyr Ala Thr Ala Gly Thr Leu Asn Glu Asp Lys
 35 40 45
 Ser Asn Ala Ile Leu Ile Pro Thr Trp Tyr Ser Gly Thr His Gln Thr
 50 55 60
 Trp Phe Gln Gln Tyr Ile Gly Thr Asp His Ala Leu Asp Pro Ser Lys
 65 70 75 80
 Tyr Phe Ile Ile Ser Ile Asn Gln Ile Gly Asn Gly Leu Ser Val Ser
 85 90 95
 Pro Ala Asn Thr Ala Asp Asp Ser Ile Ser Met Ser Lys Phe Pro Asn
 100 105 110
 Val Arg Ile Gly Asp Asp Val Val Ala Gln Asp Arg Leu Leu Arg Gln
 115 120 125
 Glu Phe Gly Ile Thr Glu Leu Phe Ala Val Val Gly Gly Ser Met Gly
 130 135 140
 Ala Gln Gln Thr Tyr Glu Trp Ile Val Arg Phe Pro Asp Gln Val His
 145 150 155 160
 Arg Ala Ala Pro Ile Ala Gly Thr Ala Lys Asn Thr Pro His Asp Phe
 165 170 175
 Ile Phe Thr Gln Thr Leu Asn Glu Thr Val Glu Ala Asp Pro Gly Phe
 180 185 190
 Asn Gly Gly Glu Tyr Ser Ser His Glu Glu Val Ala Asp Gly Leu Arg
 195 200 205

Arg Gln Ser His Leu Trp Ala Ala Met Gly Phe Ser Thr Glu Phe Trp
210 215 220

Lys Gln Glu Ala Trp Arg Arg Leu Gly Leu Glu Ser Lys Glu Ser Val
225 230 235 240

Leu Ala Asp Phe Leu Asp Pro Leu Phe Met Ser Met Asp Pro Asn Thr
245 250 255

Leu Leu Asn Asn Ala Trp Lys Trp Gln His Gly Asp Val Ser Arg His
260 265 270

Thr Gly Gly Asp Leu Ala Ala Ala Leu Gly Arg Val Lys Ala Lys Thr
275 280 285

Phe Val Met Pro Ile Ser Glu Asp Met Phe Phe Pro Val Arg Asp Cys
290 295 300

Ala Ala Glu Gln Ala Leu Ile Pro Gly Ser Glu Leu Arg Val Ile Glu
305 310 315 320

Asp Ile Ala Gly His Leu Gly Leu Phe Asn Val Ser Glu Asn Tyr Ile
325 330 335

Pro Gln Ile Asp Lys Asn Leu Lys Glu Leu Phe Glu Ser
340 345

<210> 71

<211> 1254

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (131)..(1231)

<223> RXN00403

<400> 71

tttttcagac tcttgagaat gcaaaactaga ctgacacagag ctgtccatat aaactggacg 60

aagtttttagt ctgtgccacc cagaacaggc ggttatcttc atg ccc acc ctc gcg 115
Met Pro Thr Leu Ala
1 5

cct tca ggt caa ctt gaa atc caa gcg atc ggt gat gtc tcc acc gaa 163
Pro Ser Gly Gln Leu Glu Ile Gln Ala Ile Gly Asp Val Ser Thr Glu
10 15 20

gcc gga gca atc att aca aac gct gaa atc gcc tat cac cgc tgg ggt 211
Ala Gly Ala Ile Ile Thr Asn Ala Glu Ile Ala Tyr His Arg Trp Gly
25 30 35

gaa tac cgc gta gat aaa gaa gga cgc agc aat gtc gtt ctc atc gaa 259
Glu Tyr Arg Val Asp Lys Glu Gly Arg Ser Asn Val Val Leu Ile Glu
40 45 50

cac gcc ctc act gga gat tcc aac gca gcc gat tgg tgg gct gac ttg 307
His Ala Leu Thr Gly Asp Ser Asn Ala Ala Asp Trp Trp Ala Asp Leu
55 60 65

ctc ggt ccc ggc aaa gcc atc aac act gat att tac tgc gtg atc tgt	355
Leu Gly Pro Gly Lys Ala Ile Asn Thr Asp Ile Tyr Cys Val Ile Cys	
70 75 80 85	
acc aac gtc atc ggt ggt tgc aac ggt tcc aac gga cct ggc tcc atg	403
Thr Asn Val Ile Gly Gly Cys Asn Gly Ser Thr Gly Pro Gly Ser Met	
90 95 100	
cat cca gat gga aat ttc tgg ggt aat cgc ttc ccc gcc acg tcc att	451
His Pro Asp Gly Asn Phe Trp Gly Asn Arg Phe Pro Ala Thr Ser Ile	
105 110 115	
ogt gat cag gta aac gcc gaa aaa caa ttc ctc gac gca ctc ggc atc	499
Arg Asp Gln Val Asn Ala Glu Lys Gln Phe Leu Asp Ala Leu Gly Ile	
120 125 130	
acc acg gtc gcc gca gta ctt ggt ggt tcc atg ggt ggt ggt ggt aac	547
Thr Thr Val Ala Ala Val Leu Gly Gly Ser Met Gly Gly Ala Arg Thr	
135 140 145	
cta gag tgg jcc gga arg tac cta gaa aat gtc ggc gca gtt gtt gtt	595
Leu Glu Trp Ala Ala Met Tyr Pro Gln Thr Val Gly Ala Ala Ala Val	
150 155 160 165	
cta gca gtt ttt gca cgc gcc agc gcc tgg caa atc ggc att caa tcc	643
Leu Ala Val Ser Ala Arg Ala Ser Ala Trp Gln Ile Gly Ile Gln Ser	
170 175 180	
gcc caa att aag ggc att gaa aac gac cac cac tgg cac gaa ggc aat	691
Ala Gln Ile Lys Ala Ile Glu Asn Asp His His Trp His Gln Gly Asn	
185 190 195	
tac tac gaa tcc ggt tgc aac cca gcc acc gga ctc ggc gcc gcc gga	739
Tyr Tyr Glu Ser Gly Cys Asn Pro Ala Thr Gly Leu Gly Ala Ala Arg	
200 205 210	
ggc atc gcc cac ctc acc tac cgt ggc gaa cta gaa atc gac gaa cgc	787
Arg Ile Ala His Leu Thr Tyr Arg Gly Glu Leu Glu Ile Asp Glu Arg	
215 220 225	
ttc ggc acc aaa gcc caa aag aac gaa aac cca ctc ggt ccc tac cgc	835
Phe Gly Thr Lys Ala Gln Lys Asn Glu Asn Pro Leu Gly Pro Tyr Arg	
230 235 240 245	
aag ccc gac cag cgc ttc gcc gtg gaa tcc tac ttg gac tac caa gca	883
Lys Pro Asp Gln Arg Phe Ala Val Glu Ser Tyr Leu Asp Tyr Gln Ala	
250 255 260	
gac aag cta gta cag cgt ttc gac gcc ggc tcc tac gtc ttg ctc acc	931
Asp Lys Leu Val Gln Arg Phe Asp Ala Gly Ser Tyr Val Leu Leu Thr	
265 270 275	
gac gcc ctc aac cgc cac gac att ggt cgc gac cgc gga ggc ctc aac	979
Asp Ala Leu Asn Arg His Asp Ile Gly Arg Asp Arg Gly Gly Leu Asn	
280 285 290	
aag gca ctc gaa tcc atc aaa gtt cca gtc ctt gtc gca ggc gta gat	1027
Lys Ala Leu Glu Ser Ile Lys Val Pro Val Leu Val Ala Gly Val Asp	
295 300 305	

acc gat att ttg tac ccc tac cac cag caa gaa cac ctc tcc aga aac 1075
 Thr Asp Ile Leu Tyr Pro Tyr His Gln Gln Glu His Leu Ser Arg Asn
 310 315 320 325

ctg gga aat cta ctg gca atg gca aaa atc gta tcc cct gtc ggc cac 1123
 Leu Gly Asn Leu Leu Ala Met Ala Lys Ile Val Ser Pro Val Gly His
 330 335 340

gat ggt ttc ctc acc gaa agc agc caa atg gat cgc atc gtg agg aac 1171
 Asp Ala Phe Leu Thr Glu Ser Arg Gln Met Asp Arg Ile Val Arg Asn
 345 350 355

ttc ttc agc ctc atc tcc cca gag gaa gag aac cct tgg acc tac atc 1219
 Phe Phe Ser Leu Ile Ser Pro Asp Glu Asp Asn Pro Ser Thr Tyr Ile
 360 365 370

gag ttc tac atc taataggtat ttacgacaaa ta; 1254
 Glu Phe Tyr Ile
 375

<210> 72

<211> 377

<212> PRT

<213> Corynebacterium glutamicum

<400> 72

Met Pro Thr Leu Ala Pro Ser Gly Gln Leu Glu Ile Gln Ala Ile Gly
 1 5 10 15

Asp Val Ser Thr Glu Ala Gly Ala Ile Ile Thr Asn Ala Glu Ile Ala
 20 25 30

Tyr His Arg Trp Gly Glu Tyr Arg Val Asp Lys Glu Gly Arg Ser Asn
 35 40 45

Val Val Leu Ile Glu His Ala Leu Thr Gly Asp Ser Asn Ala Ala Asp
 50 55 60

Trp Trp Ala Asp Leu Leu Gly Pro Gly Lys Ala Ile Asn Thr Asp Ile
 65 70 75 80

Tyr Cys Val Ile Cys Thr Asn Val Ile Gly Gly Cys Asn Gly Ser Thr
 85 90 95

Gly Pro Gly Ser Met His Pro Asp Gly Asn Phe Trp Gly Asn Arg Phe
 100 105 110

Pro Ala Thr Ser Ile Arg Asp Gln Val Asn Ala Glu Lys Gln Phe Leu
 115 120 125

Asp Ala Leu Gly Ile Thr Thr Val Ala Ala Val Leu Gly Gly Ser Met
 130 135 140

Gly Gly Ala Arg Thr Leu Glu Trp Ala Ala Met Tyr Pro Glu Thr Val
 145 150 155 160

Gly Ala Ala Ala Val Leu Ala Val Ser Ala Arg Ala Ser Ala Trp Gln
 165 170 175

Ile Gly Ile Gln Ser Ala Gln Ile Lys Ala Ile Glu Asn Asp His His

180

185

190

Trp His Glu Gly Asn Tyr Tyr Glu Ser Gly Cys Asn Pro Ala Thr Gly
195 200 205

Leu Gly Ala Ala Arg Arg Ile Ala His Leu Thr Tyr Arg Gly Glu Leu
210 215 220

Glu Ile Asp Glu Arg Phe Gly Thr Lys Ala Gln Lys Asn Glu Asn Pro
225 230 235 240

Leu Gly Pro Tyr Arg Lys Pro Asp Gln Arg Phe Ala Val Gln Ser Tyr
245 250 255

Leu Asp Tyr Gln Ala Asp Lys Leu Val Gln Arg Phe Asp Ala Gly Ser
260 265 270

Tyr Val Leu Leu Thr Asp Ala Leu Asn Arg His Asp Ile Gly Arg Asp
275 280 285

Arg Gly Gly Leu Asn Lys Ala Leu Glu Ser Ile Lys Val Pro Val Leu
290 295 300

Val Ala Gly Val Asp Thr Asp Ile Leu Tyr Pro Tyr His Gln Gln Glu
305 310 315 320

His Leu Ser Arg Asn Leu Gly Asn Leu Leu Ala Met Ala Lys Ile Val
325 330 335

Ser Pro Val Gly His Asp Ala Phe Leu Thr Glu Ser Arg Gln Met Asp
340 345 350

Arg Ile Val Arg Asn Phe Phe Ser Leu Ile Ser Pro Asp Glu Asp Asn
355 360 365

Pro Ser Thr Tyr Ile Glu Phe Tyr Ile
370 375

<210> 73

<211> 1210

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1210)

<223> FRXA00403

<400> 73

tttttcagac tegtgagaat gcaaaactaga ctgacacagag ctgtccatat adactggagc 60

aagtttttagt cttgtccacc cagaacaggc ggttattttc atg ccc acc ctc ggc 115
Met Pro Thr Leu Ala
1 5

cct tca ggt caa ctt gaa atc caa ggc atc ggt gat gtc tcc acc gaa 163
Pro Ser Gly Gln Leu Glu Ile Gln Ala Ile Gly Asp Val Ser Thr Glu
10 15 20

gac gga gaa atc att aca aac gat gaa atc gcc tat cac cgc tgg ggt 211

Ala Gly Ala Ile Ile Thr Asn Ala Glu Ile Ala Tyr His Arg Trp Gly
 25 30 35

gaa tac cgc gta gat aaa gaa gga cgc agc aat gtc gtt ctc atc gaa 259
 Glu Tyr Arg Val Asp Lys Glu Gly Arg Ser Asn Val Val Leu Ile Glu
 40 45 50

cac gcc ctc act gga gat tcc aac gca gcc gat tgg tgg gct gac ttg 307
 His Ala Leu Thr Gly Asp Ser Asn Ala Ala Asp Trp Trp Ala Asp Leu
 55 60 65

ctc ggt ccc gcc aaa gcc atc aac act gat att tac tgc gtg atc tgt 355
 Leu Gly Pro Gly Lys Ala Ile Asn Thr Asp Ile Tyr Cys Val Ile Cys
 70 75 80 85

acc aac gtc atc ggt ggt tgc aac gct tcc aac gga cct gcc tcc atg 403
 Thr Asn Val Ile Gly Gly Cys Asn Gly Ser Thr Gly Pro Gly Ser Met
 90 95 100

cat cca gat gga aac ttc tgg gct aat cgc ttc ccc gcc aag tcc att 451
 His Pro Asp Gly Asn Phe Trp Gly Asn Arg Phe Pro Ala Thr Ser Ile
 105 110 115

cgt gat cag gta aac gcc gaa aac cca ttc ctc gac gga ctc gcc atc 499
 Arg Asp Gln Val Asn Ala Glu Lys Gln Phe Ile Asp Ala Leu Gly Ile
 120 125 130

acc aag gtc gcc gca gta ctt ggt ggt tcc atg ggt ggt gcc cgc acc 547
 Thr Thr Val Ala Ala Val Leu Gly Gly Ser Met Gly Gly Ala Arg Thr
 135 140 145

cta gag tgg gcc gca atg tac cca gaa aat gtt gcc gca gct gct gtt 595
 Leu Glu Trp Ala Ala Met Tyr Pro Glu Thr Val Gly Ala Ala Ala Val
 150 155 160 165

ctt gca gtt tct gca cgc gcc agc gcc tgg aac atc gcc att caa tcc 643
 Leu Ala Val Ser Ala Arg Ala Ser Ala Trp Gln Ile Gly Ile Gln Ser
 170 175 180

gcc caa att aag gag att gaa aac gac cac cac tgg cac gaa gcc aac 691
 Ala Gln Ile Lys Ala Ile Glu Asn Asp His His Trp His Glu Gly Asn
 185 190 195

tac tac gaa ttc gcc tgc aac cca gcc acc gga ctc gcc gcc gcc cga 739
 Tyr Tyr Glu Ser Gly Cys Asn Pro Ala Thr Gly Leu Gly Ala Ala Arg
 200 205 210

cgc atc gcc cac ctc acc tac cgt gcc gaa cta gaa atc gac gaa cgc 787
 Arg Ile Ala His Leu Thr Tyr Arg Gly Glu Ile Glu Ile Asp Glu Arg
 215 220 225

ttc gcc acc aaa gcc caa aag aac gaa aac cca ctc ggt ccc tac cgc 835
 Phe Gly Thr Lys Ala Gln Lys Asn Glu Asn Pro Leu Gly Pro Tyr Arg
 230 235 240 245

aag ccc gac cag cgc ttc gcc gtg gaa tcc tac ttg gac tac caa gca 883
 Lys Pro Asp Gln Arg Phe Ala Val Glu Ser Tyr Leu Asp Tyr Gln Ala
 250 255 260

gac aag cta gta cag cgt ttc gac gcc gcc tcc tac gtc ttg ctc acc 931
 Asp Lys Ile Val Gln Arg Phe Asp Ala Gly Ser Tyr Val Leu Leu Thr

265

270

275

gac gcc ctc aac cgc cac gac att ggt cgc gac cgc gga ggc ctc aac 979
 Asp Ala Leu Asn Arg His Asp Ile Gly Arg Asp Arg Gly Gly Leu Asn
 280 285 290

aag gca ctc gaa tcc atc aaa gtt cca gtc ctt gtc gca ggc gta gat 1027
 Lys Ala Leu Glu Ser Ile Lys Val Pro Val Leu Val Ala Gly Val Asp
 295 300 305

acc gat att ttg tac ccc tac cac cag caa gaa cac ctc tcc aga aac 1075
 Thr Asp Ile Leu Tyr Pro Tyr His Gln Gln Glu His Leu Ser Arg Asn
 310 315 320 325

ctg gga aat cta ctg gca atg gca aaa atc gta tcc cct ctc ggc cac 1123
 Leu Gly Asn Leu Leu Ala Met Ala Lys Ile Val Ser Pro Val Gly His
 330 335 340

gat ggt ttc ctt aac gaa agc cgt caa atg gat cgc atc ctc aga aac 1171
 Asp Ala Phe Leu Thr Glu Ser Arg Gln Met Asp Arg Ile Val Arg Asn
 345 350 355

ttc ttc agc ctt atc ttc cca gac gaa gac aac ctt tgg 1210
 Phe Phe Ser Leu Ile Ser Pro Asp Glu Asp Asn Pro Ser
 360 365 370

<210> 74

<211> 370

<212> PRT

<213> Corynebacterium glutamicum

<400> 74

Met Pro Thr Leu Ala Pro Ser Gly Gln Leu Glu Ile Gln Ala Ile Gly
 1 5 10 15

Asp Val Ser Thr Glu Ala Gly Ala Ile Ile Thr Asn Ala Glu Ile Ala
 20 25 30

Tyr His Arg Trp Gly Glu Tyr Arg Val Asp Lys Glu Gly Arg Ser Asn
 35 40 45

Val Val Leu Ile Glu His Ala Leu Thr Gly Asp Ser Asn Ala Ala Asp
 50 55 60

Trp Trp Ala Asp Leu Leu Gly Pro Gly Lys Ala Ile Asn Thr Asp Ile
 65 70 75 80

Tyr Cys Val Ile Cys Thr Asn Val Ile Gly Gly Cys Asn Gly Ser Thr
 85 90 95

Gly Pro Gly Ser Met His Pro Asp Gly Asn Phe Trp Gly Asn Arg Phe
 100 105 110

Pro Ala Thr Ser Ile Arg Asp Gln Val Asn Ala Glu Lys Gln Phe Leu
 115 120 125

Asp Ala Leu Gly Ile Thr Thr Val Ala Ala Val Leu Gly Gly Ser Met
 130 135 140

Gly Gly Ala Arg Thr Leu Glu Trp Ala Ala Met Tyr Pro Glu Thr Val

145

150

155

160

Gly Ala Ala Ala Val Leu Ala Val Ser Ala Arg Ala Ser Ala Trp Gln
165 170 175

Ile Gly Ile Gln Ser Ala Gln Ile Lys Ala Ile Glu Asn Asp His His
180 185 190

Trp His Glu Gly Asn Tyr Tyr Glu Ser Gly Cys Asn Pro Ala Thr Gly
195 200 205

Leu Gly Ala Ala Arg Arg Ile Ala His Leu Thr Tyr Arg Gly Glu Leu
210 215 220

Glu Ile Asp Glu Arg Phe Gly Thr Lys Ala Gln Lys Asn Glu Asn Pro
225 230 235 240

Leu Gly Pro Tyr Arg Lys Pro Asp Gln Arg Phe Ala Val Glu Ser Tyr
245 250 255

Leu Asp Tyr Gln Ala Asp Lys Leu Val Gln Arg Phe Asp Ala Gly Ser
260 265 270

Tyr Val Leu Leu Thr Asp Ala Leu Asn Arg His Asp Ile Gly Arg Asp
275 280 285

Arg Gly Gly Leu Asn Lys Ala Leu Glu Ser Ile Lys Val Pro Val Leu
290 295 300

Val Ala Gly Val Asp Thr Asp Ile Leu Tyr Pro Tyr His Gln Gln Glu
305 310 315 320

His Leu Ser Arg Asn Leu Gly Asn Leu Leu Ala Met Ala Lys Ile Val
325 330 335

Ser Pro Val Gly His Asp Ala Phe Leu Thr Glu Ser Arg Gln Met Asp
340 345 350

Arg Ile Val Arg Asn Phe Phe Ser Leu Ile Ser Pro Asp Glu Asp Asn
355 360 365

Pic Ser
370

0210 75

0211 887

0212 DNA

0213 Corynebacterium glutamicum

0220

0221 CDS

0222 (101)..(664)

0223 EX303158

0400 75

caaaagctcac cgaaggcac aacgccaagt tggttgttga caaacaccttg gcacccccat 60

acctgcagca gccactaaaa ctgggcgcac acgcaagtcc ttg cac tcc acc acc 115
Leu His Ser Thr Thr

1

5

aag tac atc gaa gga cac tcc gac gtt gtt ggc ggc ctt gtg ggt acc 163
 Lys Tyr Ile Glu Gly His Ser Asp Val Val Gly Gly Leu Val Gly Thr
 10 15 20
 aac gac cag gaa atg gac gaa gaa cag cag ttc atg cag ggc ggc atc 211
 Asn Asp Gln Glu Met Asp Glu Glu Leu Leu Phe Met Gln Gly Gly Ile
 25 30 35
 gga cag atc cca tca gtt ttc gat gca tac ctg acc gcc cgt ggc ctc 259
 Gly Pro Ile Pro Ser Val Phe Asp Ala Tyr Leu Thr Ala Arg Gly Leu
 40 45 50
 aag acc ctt gca gtg cgc atg gat cgc cac tgc gac aac gca gaa aag 307
 Lys Thr Leu Ala Val Arg Met Asp Arg His Cys Asp Asn Ala Glu Lys
 55 60 65
 atc gcc gaa ttc cag gac tcc cgc cca gag gtc tcc acc gtg ctc tac 355
 Ile Ala Glu Phe Leu Asp Ser Arg Pro Glu Val Ser Thr Val Leu Tyr
 70 75 80
 cca ggt cag aag aac cac cca ggc cac gaa gtc gca ggc aag cag atg 403
 Pro Gly Leu Lys Asn His Pro Gly His Glu Val Ala Ala Lys Gln Met
 85 90 95 100
 aag cgc ttc ggc ggc atg atc tcc gtc cgt ttc gca ggc ggc gaa gaa 451
 Lys Arg Phe Gly Gly Met Ile Ser Val Arg Phe Ala Gly Gly Glu Glu
 105 110 115
 gaa cct aag aag ttc tgt acc tcc acc aac ctg atc tgt ctg gcc gag 499
 Ala Ala Lys Lys Phe Cys Thr Ser Thr Lys Leu Ile Cys Leu Ala Glu
 120 125 130
 ttc ctc ggt ggc gtg gaa tcc ctc ctg gag cac cca gca acc atg acc 547
 Ser Leu Gly Gly Val Glu Ser Leu Leu Glu His Pro Ala Thr Met Thr
 135 140 145
 ctc cag tca gct gcc ggc tct cag ctc gag gtt ccc cgc gac ctc gtg 595
 His Gln Ser Ala Ala Gly Ser Gln Leu Glu Val Pro Arg Asp Leu Val
 150 155 160 165
 cgc atc tcc att ggt att gaa gac att gaa gac ctg ctc gca gat gtc 643
 Arg Ile Ser Ile Gly Ile Glu Asp Ile Glu Asp Leu Leu Ala Asp Val
 170 175 180
 gag cag gcc ctc aat aac ctt tagaaactat ttggcggcaa gca 687
 Glu Gln Ala Leu Asn Asn Leu
 185

12100-76

1110-188

112-PST

113-Corynebacterium glutamicum

1400-76

Leu His Ser Thr Thr Lys Tyr Ile Glu Gly His Ser Asp Val Val Gly
 1 5 10 15

Gly Leu Val Gly Thr Asn Asp Gln Glu Met Asp Glu Glu Leu Leu Phe
 20 25 30

Met Gln Gly Gly Ile Gly Pro Ile Pro Ser Val Phe Asp Ala Tyr Leu
 35 40 45

Thr Ala Arg Gly Leu Lys Thr Leu Ala Val Arg Met Asp Arg His Cys
 50 55 60

Asp Asn Ala Glu Lys Ile Ala Glu Phe Leu Asp Ser Arg Pro Glu Val
 65 70 75 80

Ser Thr Val Leu Tyr Pro Gly Leu Lys Asn His Pro Gly His Glu Val
 85 90 95

Ala Ala Lys Gln Met Lys Arg Phe Gly Gly Met Ile Ser Val Arg Phe
 100 105 110

Ala Gly Gly Glu Glu Ala Ala Lys Lys Phe Cys Thr Ser Thr Lys Leu
 115 120 125

Ile Cys Leu Ala Glu Ser Leu Gly Gly Val Glu Ser Leu Leu Glu His
 130 135 140

Pro Ala Thr Met Thr His Gln Ser Ala Ala Gly Ser Gln Leu Glu Val
 145 150 155 160

Pro Arg Asp Leu Val Arg Ile Ser Ile Gly Ile Glu Asp Ile Glu Asp
 165 170 175

Ile Leu Ala Asp Val Glu Gln Ala Leu Asn Asn Leu
 180 185

<210> 77

<211> 617

<212> DNA

<213> Corynebacterium glutamicum

0220

0221: CDS

0222: (1)..(594)

0223: FRXAG0254

<400> 77

cag cca cta aaa ctc ggc gca cac gca gtc ttg cac tcc acc acc aag 48
 Gln Pro Leu Lys Leu Gly Ala His Ala Val Leu His Ser Thr Thr Lys
 1 5 10 15

tac atc gga gga cac tcc gac gtt gtt ggc ggc ctt gtg gtt acc aac 96
 Tyr Ile Gly Gly His Ser Asp Val Val Gly Gly Leu Val Val Thr Asn
 20 25 30

gac cag gaa atg gac gaa gaa ctg ctg ttc atg cag ggc ggc atc gga 144
 Asp Gln Glu Met Asp Glu Glu Leu Leu Phe Met Gln Gly Gly Ile Gly
 35 40 45

cag atc cca tca gtt ttc gat gca tac ctg acc gcc cgt ggc ctc aag 192
 Pro Ile Pro Ser Val Phe Asp Ala Tyr Leu Thr Ala Arg Gly Leu Lys
 50 55 60

acc ctt gca gtg cgc atg gat cgc cac tgc gac aac gca gaa aag atc 240
 Thr Leu Ala Val Arg Met Asp Arg His Cys Asp Asn Ala Glu Lys Ile

80

Gly Leu Lys Asn His Pro Gly His Glu Val Ala Ala Lys Gln Met Lys
100 105 110

Arg Phe Gly Gly Met Ile Ser Val Arg Phe Ala Gly Gly Glu Glu Ala
115 120 125

Ala Lys Lys Phe Cys Thr Ser Thr Lys Leu Ile Cys Leu Ala Glu Ser
130 135 140

Leu Gly Gly Val Glu Ser Leu Leu Glu His Pro Ala Thr Met Thr His
145 150 155 160

Gln Ser Ala Ala Gly Ser Gln Leu Glu Val Pro Arg Asp Leu Val Arg
165 170 175

Ile Ser Ile Gly Ile Glu Asp Ile Glu Asp Leu Leu Ala Asp Val Glu
180 185 190

Gln Ala Leu Asn Asn Leu
195

<210> 29

<211> 1170

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> [101]...[1147]

<223> KXA02532

<400> 29

gatgaatttt tacacacact cgtacactat taacatcgag tgggtgtaac acacagtaac 60

tgtgcaagcg ggacgggcag ccagaactcc tgggtgagcg atg aac cta cct atc 115
Met Asn Pro Pro Ile
1 5

aag ttg tcc agc act tat gtt cat gat tca gaa aaa gct tat ggg cgc 163
Thr Leu Ser Ser Thr Tyr Val His Asp Ser Glu Lys Ala Tyr Gly Arg
10 15 20

gat ggc aat gat gga tgg ggt gca ttt gag gct gcc atg gga act cta 211
Asp Gly Asn Asp Gly Trp Gly Ala Phe Glu Ala Ala Met Gly Thr Leu
25 30 35

gat ggt ggg ttc ggc gta tct tat tct tca ggt ttg gca ggc gca acg 259
Asp Gly Gly Phe Ala Val Ser Tyr Ser Ser Gly Leu Ala Ala Ala Thr
40 45 50

tcg att gct gat ttg gtt cct act ggt ggc aca gtt gtt tta cct aaa 307
Ser Ile Ala Asp Leu Val Pro Thr Gly Gly Thr Val Val Leu Pro Lys
55 60 65

gct gcc tat tat ggc gtg acc aat att ttc gcc agg atg gaa gcc cgc 355
Ala Ala Tyr Tyr Gly Val Thr Asn Ile Phe Ala Arg Met Glu Ala Arg
70 75 80 85

gga agg ctg aag gtt cga act gtt gat gca gac aat acc gaa gaa gtc 403
Gly Arg Leu Lys Val Arg Thr Val Asp Ala Asp Asn Thr Glu Glu Val
90 95 100

att gct gct gct caa ggt gca gat gtg gtg tgg gtg gaa tgg atc gct Ile Ala Ala Ala Gln Gly Ala Asp Val Val Trp Val Glu Ser Ile Ala 105 110 115	451
aat ccg acg atg gtg gta gct gat atc cct gca ata gtc gac ggt gtg Asn Pro Thr Met Val Val Ala Asp Ile Pro Ala Ile Val Asp Gly Val 120 125 130	499
cgt ggg ctt gga gtt ttg act gtc gtt gac gga act ttc gca acg caa Arg Gly Leu Gly Val Leu Thr Val Val Asp Ala Thr Phe Ala Thr Pro 135 140 145	547
ctt cgt caa cgt caa ttg gaa ctt ggt gct gat att gtg ctt tac tgg Leu Arg Gln Arg Pro Leu Glu Leu Gly Ala Asp Ile Val Leu Tyr Ser 150 155 160 165	595
gca acc aaa ctt atc ggt gga caa tct gat ctt ctt ctt aga gtc gca Ala Thr Lys Leu Ile Gly Gly His Ser Asp Leu Leu Leu Gly Val Ala 170 175 180	643
gtg ttc aat ttt gag caa caa ggt tgg ttt ctt gtt act taa cgt cat Val Cys Lys Ser Glu His His Ala Gln Phe Leu Ala Thr His Arg His 185 190 195	691
gat cat ggt taa gtg ccg gga ggt ctt gaa ggt ttt ctt gct ctc cgt Asp His Gly Ser Val Pro Gly Gly Leu Glu Ala Phe Leu Ala Leu Arg 200 205 210	739
gga ttg tat tcc ttg ggg gtg cgt ctt cat aga gaa gaa tcc aat gta Gly Leu Tyr Ser Leu Ala Val Arg Leu Asp Arg Ala Glu Ser Asn Ala 215 220 225	787
gca gaa ctt tgg cgt aga ctt aat gag cat ctt tgg gtt acc cgt gtc Ala Glu Leu Ser Arg Arg Leu Asn Ala His Pro Ser Val Thr Arg Val 230 235 240 245	835
aat tat caa gga ctt cct gat gat ccc caa cat gaa aaa gcc gtg cga Asn Tyr Pro Gly Leu Pro Asp Asp Pro Gln His Glu Lys Ala Val Arg 250 255 260	883
gtc eta ccc tct gga tgt gga aac atg ttg tca ttt gag ctt gat gca Val Leu Pro Ser Gly Cys Gly Asn Met Leu Ser Phe Glu Leu Asp Ala 265 270 275	931
aca cct gaa cga act gat gag att ctc gaa agc ctg tca ctt tta acc Thr Pro Glu Arg Thr Asp Glu Ile Leu Glu Ser Leu Ser Leu Leu Thr 280 285 290	979
cac gcg acc agt tgg gga ggt gtg gaa aca gcc att gaa cgt cgc acc His Ala Thr Ser Trp Gly Gly Val Glu Thr Ala Ile Glu Arg Arg Thr 295 300 305	1027
agg cgg gat gct gaa gtg gtg gca gaa gta ccg atg act ctt tgc cgc Arg Arg Asp Ala Glu Val Val Ala Glu Val Pro Met Thr Leu Cys Arg 310 315 320 325	1075
gtt tcc gta gga att gaa gac gtt gaa gat cta tgg gaa gac ctc aac Val Ser Val Gly Ile Glu Asp Val Glu Asp Leu Trp Glu Asp Leu Asn 330 335 340	1123
gcc tca atc gac aaa gtt ctg ggt tagaaactcgt agccagtaac cag	1170

Ala Ser Ile Asp Lys Val Leu Gly
345

<210> 80

<211> 349

<212> PRT

<213> Corynebacterium glutamicum

<400> 80

Met Asn Pro Pro Ile Thr Leu Ser Ser Thr Tyr Val His Asp Ser Glu
1 5 10 15

Lys Ala Tyr Gly Arg Asp Gly Asn Asp Gly Trp Gly Ala Phe Glu Ala
20 25 30

Ala Met Gly Thr Leu Asp Gly Gly Phe Ala Val Ser Tyr Ser Ser Gly
35 40 45

Leu Ala Ala Ala Thr Ser Ile Ala Asp Leu Val Pro Thr Gly Gly Thr
50 55 60

Val Val Leu Pro Lys Ala Ala Tyr Tyr Gly Val Thr Asn Ile Phe Ala
65 70 75 80

Arg Met Glu Ala Arg Gly Arg Leu Lys Val Arg Thr Val Asp Ala Asp
85 90 95

Asn Thr Glu Glu Val Ile Ala Ala Ala Gln Gly Ala Asp Val Val Trp
100 105 110

Val Glu Ser Ile Ala Asn Pro Thr Met Val Val Ala Asp Ile Pro Ala
115 120 125

Ile Val Asp Gly Val Arg Gly Leu Gly Val Leu Thr Val Val Asp Ala
130 135 140

Phe Phe Ala Thr Pro Leu Arg Gln Arg Pro Leu Glu Leu Gly Ala Asp
145 150 155 160

Ile Val Leu Tyr Ser Ala Thr Lys Leu Ile Gly Gly His Ser Asp Leu
165 170 175

Leu Leu Gly Val Ala Val Cys Lys Ser Glu His His Ala Gln Phe Leu
180 185 190

Ala Thr His Arg His Asp His Gly Ser Val Pro Gly Gly Leu Glu Ala
195 200 205

Phe Leu Ala Leu Arg Gly Leu Tyr Ser Leu Ala Val Arg Leu Asp Arg
210 215 220

Ala Glu Ser Asn Ala Ala Glu Leu Ser Arg Arg Leu Asn Ala His Pro
225 230 235 240

Ser Val Thr Arg Val Asn Tyr Pro Gly Leu Pro Asp Asp Pro Gln His
245 250 255

Glu Lys Ala Val Arg Val Leu Pro Ser Gly Cys Gly Asn Met Leu Ser
260 265 270

Phe Glu Leu Asp Ala Thr Pro Glu Arg Thr Asp Glu Ile Leu Glu Ser
 275 280 285

Leu Ser Leu Leu Thr His Ala Thr Ser Trp Gly Gly Val Glu Thr Ala
 290 295 300

Ile Glu Arg Arg Thr Arg Arg Asp Ala Glu Val Val Ala Glu Val Pro
 305 310 315 320

Met Thr Leu Cys Arg Val Ser Val Gly Ile Glu Asp Val Glu Asp Leu
 325 330 335

Trp Glu Asp Leu Asn Ala Ser Ile Asp Lys Val Leu Gly
 340 345

<210> 41
 <211> 861
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(838)
 <223> K01381.1

<240> 41
 agggggtat tttacacaaa agtggacacg ttgtgtatat attgacagaa gacgggtcct 60

tttagggcca ttagaattctg attacaggag ttgatctacc ttg tct ttt gac cca 115
 Leu Ser Ile Asp Pro
 1 5

aac acc cag ggt ttc tcc act gca tgg att caa gct ggg tat gag cca 163
 Asn Thr Gln Gly Phe Ser Thr Ala Ser Ile His Ala Gly Tyr Glu Pro
 10 15 20

gac gac tac tac ggt tgg att aac acc cca atc tat gcc tcc acc acc 211
 Asp Asp Tyr Tyr Gly Ser Ile Asn Thr Pro Ile Tyr Ala Ser Thr Thr
 25 30 35

ttc gcg cag aac gct cca aac gaa ctg cgc aaa ggc tac gag tac acc 259
 Phe Ala Gln Asn Ala Pro Asn Glu Leu Arg Lys Gly Tyr Glu Tyr Thr
 40 45 50

cgt gtg ggc aac ccc acc atc gtg gca tta gag cag acc gtc gca gca 307
 Arg Val Gly Asn Pro Thr Ile Val Ala Leu Glu Gln Thr Val Ala Ala
 55 60 65

ctc gaa ggc gca aag tat ggc cgc gca ttc tcc tcc ggc atg gct gca 355
 Leu Glu Gly Ala Lys Tyr Gly Arg Ala Phe Ser Ser Gly Met Ala Ala
 70 75 80 85

acc gac atc ctg ttc cgc atc atc ctc aag ccg ggc gat caa atc gtc 403
 Thr Asp Ile Leu Phe Arg Ile Ile Leu Lys Pro Gly Asp His Ile Val
 90 95 100

ctc ggc aac gat gct tac ggc gga acc tac cgc ctg atc gac acc gta 451
 Leu Gly Asn Asp Ala Tyr Gly Gly Thr Tyr Arg Leu Ile Asp Thr Val
 105 110 115

ttc acc gca tgg ggc gtc gaa tac acc gtt gtt gat acc tcc gtc gtg 499
Phe Thr Ala Trp Gly Val Glu Tyr Thr Val Val Asp Thr Ser Val Val
120 125 130

gaa gag gtc aag gca ggc atc aag gac aac acc aag ctg atc tgg gtg 547
Glu Glu Val Lys Ala Ala Ile Lys Asp Asn Thr Lys Leu Ile Trp Val
135 140 145

gaa acc cca acc aac cca gca ctt ggc atc acc gac atc gaa gca gta 595
Glu Thr Pro Thr Asn Pro Ala Leu Gly Ile Thr Asp Ile Glu Ala Val
150 155 160 165

gca aag ctg acc gaa ggc acc aac gcc aag tgg gtt gtt gac aac acc 643
Ala Lys Leu Thr Glu Gly Thr Asn Ala Lys Leu Val Val Asp Asn Thr
170 175 180

tig gca tcc cca tac ctg cag cag cca cta aac ctg ggc aca cac gca 691
Leu Ala Ser Pro Tyr Leu Gln Gln Pro Leu Lys Leu Gly Ala His Ala
185 190 195

agt acc tgc act cca gca cca agt aca tgg aag gac acc acc aag tgg 739
Ser Pro Cys Thr Pro Pro Pro Ser Thr Ser Lys Asp Thr Pro Thr Leu
200 205 210

tig acc gca tgg tgg gta cca acc gcc aag aac tgg acc aag aac tgg 787
Leu Ala Ala Leu Trp Val Pro Thr Thr Arg Lys Trp Thr Lys Asn Cys
215 220 225

tgt tca tgc agg ggc gca tcc gac cga tcc cat cag ttt tgg atg cat 835
Cys Ser Cys Arg Ala Ala Ser Asp Arg Ser His Gln Phe Ser Met His
230 235 240 245

acc agacagagc tggactaaag acc 881
Thr

<210> 32

<211> 246

<212> PRT

<213> Corynebacterium glutamicum

<400> 32

Leu Ser Phe Asp Pro Asn Thr Gln Gly Phe Ser Thr Ala Ser Ile His
1 5 10 15

Ala Gly Tyr Glu Pro Asp Asp Tyr Tyr Gly Ser Ile Asn Thr Pro Ile
20 25 30

Tyr Ala Ser Thr Thr Phe Ala Gln Asn Ala Pro Asn Glu Leu Arg Lys
35 40 45

Gly Tyr Glu Tyr Thr Arg Val Gly Asn Pro Thr Ile Val Ala Leu Glu
50 55 60

Gln Thr Val Ala Ala Leu Glu Gly Ala Lys Tyr Gly Arg Ala Phe Ser
65 70 75 80

Ser Gly Met Ala Ala Thr Asp Ile Leu Phe Arg Ile Ile Leu Lys Pro
85 90 95

Gly Asp His Ile Val Leu Gly Asn Asp Ala Tyr Gly Gly Thr Tyr Arg
 100 105 110

Leu Ile Asp Thr Val Phe Thr Ala Trp Gly Val Glu Tyr Thr Val Val
 115 120 125

Asp Thr Ser Val Val Glu Glu Val Lys Ala Ala Ile Lys Asp Asn Thr
 130 135 140

Lys Leu Ile Trp Val Glu Thr Pro Thr Asn Pro Ala Leu Gly Ile Thr
 145 150 155 160

Asp Ile Glu Ala Val Ala Lys Leu Thr Glu Gly Thr Asn Ala Lys Leu
 165 170 175

Val Val Asp Asn Thr Leu Ala Ser Pro Tyr Leu Gln Gln Pro Leu Lys
 180 185 190

Leu Gly Ala His Ala Ser Pro Cys Thr Pro Pro Pro Ser Thr Ser Lys
 195 200 205

Asp Thr Pro Thr Leu Leu Ala Ala Leu Trp Val Pro Thr Thr Arg Lys
 210 215 220

Trp Thr Lys Asn Cys Cys Ser Cys Arg Ala Ala Ser Asp Arg Ser His
 225 230 235 240

Gln Phe Ser Met His Thr
 245

<210> 83
 <211> 703
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(703)
 <223> FRXA02768

<220>
 <223> All occurrences of n = any nucleotide

<220>
 <223> All occurrences of Xaa = any amino acid

<400> 83
 aggggctagt ttacacaaa agtggacagc ttggtctatc attgccagaa gaccggctct 60
 tttagggcca tagaattctg attacaggag ttgatctacc ttg tct ttt gac cca 115
 Leu Ser Phe Asp Pro
 1 5

aac acc cag ggt ttc tcc act gca tcc att cac gct ggg tat gag cca 163
 Asn Thr Gln Gly Phe Ser Thr Ala Ser Ile His Ala Gly Tyr Glu Pro
 10 15 20

gac gac tac tac ggt tcc att aac acc cca atc tat gcc tcc acc acc 211
 Asp Asp Tyr Tyr Gly Ser Ile Asn Thr Pro Ile Tyr Ala Ser Thr Thr
 25 30 35

ttc ggc cag aac gct cca aac gaa ctg cgc aaa ggc tac gag tac acc 259
 Phe Ala Gln Asn Ala Pro Asn Glu Leu Arg Lys Gly Tyr Glu Tyr Thr
 40 45 50
 cgt gtg ggc aac ccc acc atc gtg gca tta gag cag acc gtc gca gca 307
 Arg Val Gly Asn Pro Thr Ile Val Ala Leu Glu Gln Thr Val Ala Ala
 55 60 65
 ctc gaa ggc gca aag tat ggc cgc gca ttc tcc tcc ggc atg gct gca 355
 Leu Glu Gly Ala Lys Tyr Gly Arg Ala Phe Ser Ser Gly Met Ala Ala
 70 75 80 85
 acc gac atc ctg ttc cgc atc atc ctc aag ccg ggc gat cag atc gtc 403
 Thr Asp Ile Leu Phe Arg Ile Ile Leu Lys Pro Gly Asp His Ile Val
 90 95 100
 ctg ggc aac tat gct tac cgc gga ttc tac cgc ctg atc gac aac gta 451
 Leu Gly Asn Asp Ala Tyr Gly Gly Thr Tyr Arg Leu Ile Asp Thr Val
 105 110 115
 ttc aac gca tgg cgc gtc gaa tac aac ttc ttc ttc aac tac ttc ctg 499
 Phe Thr Ala Trp Gly Val Glu Tyr Thr Val Val Asp Thr Ser Val Val
 120 125 130
 gaa aag gtr aac gca ggc atc aag gac ttc aac aag gtr tat ttc ttc 547
 Glu Glu Val Lys Ala Ala Ile Lys Asp Asn Thr Lys Ala Asp Leu Gly
 135 140 145
 gga aac ccc aac caa ccc agc act ttg gca tta ccc gac atc gaa gca 595
 Gly Asn Pro Asn Gln Pro Ser Thr Leu Ala Leu Pro Asp Ile Glu Ala
 150 155 160 165
 gtn tgc aaa act tca ccc gaa agg cag caa ccc caa gct tgc tgt ttg 643
 Val Cys Lys Thr Ser Pro Glu Arg His Gln Pro Gln Ala Cys Cys Leu
 170 175 180
 aca aca cct tgc cat tcc cca tac ctg cag aan caa ctt aaa ant tnn 691
 Thr Thr Pro Ser His Ser Pro Tyr Leu Gln Xaa Pro Leu Lys Xaa Xaa
 185 190 195
 gng cag acg gag 703
 Xaa His Thr Gln
 200

<210> 84

<211> 201

<212> PRT

<213> Corynebacterium glutamicum

<20>

<23> All occurrences of Xaa = any amino acid

<400> 84

Leu Ser Phe Asp Pro Asn Thr Gln Gly Phe Ser Thr Ala Ser Ile His
 1 5 10 15

Ala Gly Tyr Glu Pro Asp Asp Tyr Tyr Gly Ser Ile Asn Thr Pro Ile
 20 25 30

Tyr Ala Ser Thr Thr Phe Ala Gln Asn Ala Pro Asn Glu Leu Arg Lys
 35 40 45
 Gly Tyr Glu Tyr Thr Arg Val Gly Asn Pro Thr Ile Val Ala Leu Glu
 50 55 60
 Gln Thr Val Ala Ala Leu Glu Gly Ala Lys Tyr Gly Arg Ala Phe Ser
 65 70 75 80
 Ser Gly Met Ala Ala Thr Asp Ile Leu Phe Arg Ile Ile Leu Lys Pro
 85 90 95
 Gly Asp His Ile Val Leu Gly Asn Asp Ala Tyr Gly Gly Thr Tyr Arg
 100 105 110
 Leu Ile Asp Thr Val Phe Thr Ala Trp Gly Val Glu Tyr Thr Val Val
 115 120 125
 Asp Thr Ser Val Val Glu Glu Val Lys Ala Ala Ile Lys Asp Asn Thr
 130 135 140
 Lys Ala Asp Leu Gly Gly Asn Pro Asn Gln Pro Ser Thr Leu Ala Leu
 145 150 155 160
 Pro Asp Ile Glu Ala Val Cys Lys Thr Ser Pro Glu Arg His Gln Pro
 165 170 175
 Gln Ala Cys Cys Leu Thr Thr Pro Ser His Ser Pro Tyr Leu Glu Asa
 180 185 190
 Pro Leu Lys Asa Asa Asa His Thr Gln
 195 200

<210> 85
 <211> 1113
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1090)
 <223> RXA00216

<400> 85
 gtgttgctcg caggccaggca gcagtgtgtt acctgcctga cgggatggg gacatcgttc 60
 ttggatcagg caaccatctgc cacacggagt cttaagaaaa ttg ggc gct tat ggt 115
 Leu Gly Ala Tyr Gly
 1 5
 tta ggt gag ctt cct gga aaa tcc gcc gcc gaa gcc gcc gac att att 163
 Leu Gly Glu Leu Pro Gly Lys Ser Ala Ala Glu Ala Ala Asp Ile Ile
 10 15 20
 cag ggt gaa acg gcc gat ctt ctc cat att cct cag ctt ccg gcc cga 211
 Gln Gly Glu Thr Gly Asp Leu Leu His Ile Pro Gln Leu Pro Ala Arg
 25 30 35
 ggt ttg ggt gct gat ctg atc ggt cga acc gtc ggt ctg ctg gac atg 259
 Gly Leu Gly Ala Asp Leu Ile Gly Arg Thr Val Gly Leu Leu Asp Met

40	45	50	
atc aac gtt gat cgc ggg gcc cga tct tgg gtg atg agc aca cgc ccc			307
Ile Asn Val Asp Arg Gly Ala Arg Ser Trp Val Met Ser Thr Arg Pro			
55	60	65	
agc aga ttg acg cac ctg acc ggc gat ttc ctt gac atg gat ttg gat			355
Ser Arg Leu Thr His Leu Thr Gly Asp Phe Leu Asp Met Asp Leu Asp			
70	75	80	85
ggc tgc gag gaa acc tgg gga acg ggc gtc gac aag cta aaa atc caa			403
Ala Cys Glu Glu Thr Trp Gly Thr Gly Val Asp Lys Leu Lys Ile Gln			
90	95	100	
gtt gct ggt ccc tgg act tta ggt ggg cgt att gag ttg gcc act ggc			451
Val Ala Gly Pro Trp Thr Leu Gly Ala Arg Ile Glu Leu Ala Asn Gly			
105	110	115	
cat cgc ggt ttg tct gat cgc ggt gag atg cgt gat ctc acg tgg ggc			499
His Arg Val Leu Ser Asp Arg Gly Ala Met Arg Asp Leu Thr Gln Ala			
120	125	130	
ctg atc ggc ggc atc gat ggc cat ggt cgc aag gtt gct tgg cga ttt			547
Leu Ile Ala Gly Ile Asp Ala His Ala Arg Lys Val Ala Gly Arg Phe			
135	140	145	
agg ttc gaa gta tgg tta caa atc tat gat tgg tgg cta aaa tct att			595
Arg Ala Glu Val Gln Val Gln Ile Asp Glu Pro Glu Leu Lys Ser Leu			
150	155	160	165
atc aac ggt tct ctc cat ggc act tta acc ttt gac att att att ggc			643
Ile Asp Gly Ser Leu Pro Gly Thr Ser Thr Phe Asp Ile Ile Pro Ala			
170	175	180	
gtg aat gtc gct gat gcc agt gaa cgt ttg cag cag gtc ttt agc tgg			691
Val Asn Val Ala Asp Ala Ser Glu Arg Leu Gln Gln Val Phe Ser Ser			
185	190	195	
att gag ggg ccg aca tat ctc aac ctc acc ggc cag att cct act tgg			739
Ile Glu Gly Pro Thr Tyr Leu Asn Leu Thr Gly Gln Ile Pro Thr Trp			
200	205	210	
gat gtg gct cgg ggt ggc ggc gcc gat act gtg cag att tcc atg gat			787
Asp Val Ala Arg Gly Ala Gly Ala Asp Thr Val Gln Ile Ser Met Asp			
215	220	225	
caa gtc cgt gga aat gaa cat ttg gat ggt ttt ggt gaa acc atc acc			835
Gln Val Arg Gly Asn Glu His Leu Asp Gly Phe Gly Glu Thr Ile Thr			
230	235	240	245
agt gga att cgt ctt ggt ttg ggc att acg aca gga aaa gat gtc gta			883
Ser Gly Ile Arg Leu Gly Leu Gly Ile Thr Thr Gly Lys Asp Val Val			
250	255	260	
gat gaa ctg ctc gag cga ccg cgg caa aag gcc gtt gag gta gaa cgc			931
Asp Glu Leu Leu Glu Arg Pro Arg Gln Lys Ala Val Glu Val Ala Arg			
265	270	275	
ttt ttt gat cgt tta ggt gtg ggc cga aac tat ctc gtg gat gct gtt			979
Phe Phe Asp Arg Leu Gly Val Gly Arg Asn Tyr Leu Val Asp Ala Val			
280	285	290	

gat att cat ccg ggt gag gat ttg gtg cag ggg acc atc acc gag gcc 1027
 Asp Ile His Pro Gly Glu Asp Leu Val Gln Gly Thr Ile Thr Glu Ala
 295 300 305

ggg cag ggt tat cgc atg gcc cgg gtg atg tgg gag atg ttg tgg aag 1075
 Ala Gln Ala Tyr Arg Met Ala Arg Val Met Ser Glu Met Leu Ser Lys
 310 315 320 325

gat tca tgc gac ctt taaggcttta cggggctggg gtt 1113
 Asp Ser Cys Asp Leu
 330

<210> 86

<211> 330

<212> PRT

<213> Corynebacterium glutamicum

<400> 86

Leu Gly Ala Tyr Gly Leu Gly Glu Leu Pro Gly Lys Ser Ala Ala Glu
 1 5 10 15

Ala Ala Asp Ile Ile Gln Gly Glu Thr Gly Asp Leu Leu His Ile Pro
 20 25 30

Gln Leu Pro Ala Arg Gly Leu Gly Ala Asp Leu Ile Gly Arg Thr Val
 35 40 45

Gly Leu Leu Asp Met Ile Asn Val Asp Arg Gly Ala Arg Ser Trp Val
 50 55 60

Met Ser Thr Arg Pro Ser Arg Leu Thr His Leu Thr Gly Asp Phe Leu
 65 70 75 80

Asp Met Asp Leu Asp Ala Cys Glu Gln Thr Trp Gly Thr Gly Val Asp
 85 90 95

Lys Leu Lys Ile Gln Val Ala Gly Pro Trp Thr Leu Gly Ala Arg Ile
 100 105 110

Glu Leu Ala Asn Gly His Arg Val Leu Ser Asp Arg Gly Ala Met Arg
 115 120 125

Asp Leu Thr Gln Ala Leu Ile Ala Gly Ile Asp Ala His Ala Arg Lys
 130 135 140

Val Ala Gly Arg Phe Arg Ala Glu Val Gln Val Gln Ile Asp Glu Pro
 145 150 155 160

Glu Leu Lys Ser Leu Ile Asp Gly Ser Leu Pro Gly Thr Ser Thr Phe
 165 170 175

Asp Ile Ile Pro Ala Val Asn Val Ala Asp Ala Ser Glu Arg Leu Gln
 180 185 190

Gln Val Phe Ser Ser Ile Glu Gly Pro Thr Tyr Leu Asn Leu Thr Gly
 195 200 205

Gln Ile Pro Thr Trp Asp Val Ala Arg Gly Ala Gly Ala Asp Thr Val
 210 215 220

Gln Ile Ser Met Asp Gln Val Arg Gly Asn Glu His Leu Asp Gly Phe
 225 230 235 240

Gly Glu Thr Ile Thr Ser Gly Ile Arg Leu Gly Leu Gly Ile Thr Thr
 245 250 255

Gly Lys Asp Val Val Asp Glu Leu Leu Glu Arg Pro Arg Gln Lys Ala
 260 265 270

Val Glu Val Ala Arg Phe Phe Asp Arg Leu Gly Val Gly Arg Asn Tyr
 275 280 285

Leu Val Asp Ala Val Asp Ile His Pro Gly Glu Asp Leu Val Gln Gly
 290 295 300

Thr Ile Thr Glu Ala Ala Gln Ala Tyr Arg Met Ala Arg Val Met Ser
 305 310 315 320

Glu Met Leu Ser Lys Asp Ser Cys Asp Leu
 325 330

<210> 87
 <211> 551
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (1)..(528)
 <223> RXA02197

<400> 87
 ggc gaa cgc atg cgc ttt agc ttc cca agc cag cag agc ggc agc ttc 48
 Ala Glu Arg Met Arg Phe Ser Phe Pro Arg Gln Gln Arg Gly Arg Phe
 1 5 10 15

ttg tgc atc gag gat ttc att cgc cca cgc gag caa gct gtc aag gac 96
 Leu Cys Ile Ala Asp Phe Ile Arg Pro Arg Glu Gln Ala Val Lys Asp
 20 25 30

ggc caa gtg gac gtc atg cca ttc cag ctg gtc acc atg ggt aat cct 144
 Gly Gln Val Asp Val Met Pro Phe Gln Leu Val Thr Met Gly Asn Pro
 35 40 45

att gct gat ttc gcc aac gag ttg ttc gca gcc aat gaa tac cgc gag 192
 Ile Ala Asp Phe Ala Asn Glu Leu Phe Ala Ala Asn Glu Tyr Arg Glu
 50 55 60

tac ttg gaa gtt cac ggc atc ggc gtg cag ctc acc gaa gca ttg gcc 240
 Tyr Leu Glu Val His Gly Ile Gly Val Gln Leu Thr Glu Ala Leu Ala
 65 70 75 80

gag tac tgg cac tcc cga gtg cgc agc gaa ctc aag ctg aac gac ggt 288
 Glu Tyr Trp His Ser Arg Val Arg Ser Glu Leu Lys Leu Asn Asp Gly
 85 90 95

gga tct gtc gct gat ttt gat cca gaa gac aag acc aag ttc ttc gac 336
 Gly Ser Val Ala Asp Phe Asp Pro Glu Asp Lys Thr Lys Phe Phe Asp
 100 105 110

ctg gat tac cgc ggc gcc cgc ttc tcc ttt ggt tac ggt tct tgc cct 384
 Leu Asp Tyr Arg Gly Ala Arg Phe Ser Phe Gly Tyr Gly Ser Cys Pro
 115 120 125

gat ctg gaa gac cgc gca aag ctg gtg gaa ttg ctc gag cca ggc cgt 432
 Asp Leu Glu Asp Arg Ala Lys Leu Val Glu Leu Leu Glu Pro Gly Arg
 130 135 140

ctc ggc gtg gag ttg tcc gag gaa ctc cag ctg cag cca gag cag tcc 480
 Ile Gly Val Glu Leu Ser Glu Glu Leu Gln Leu His Pro Glu Gln Ser
 145 150 155 160

aca gag ggc ttt gtg ctc tac cac cca gag gaa aac tac ttt aac gtc 528
 Thr Asp Ala Phe Val Leu Tyr His Pro Glu Ala Lys Tyr Phe Asn Val
 165 170 175

taaacacatt gaaaggaaa act 551

<210> 11
 <211> 176
 <212> FRT
 <213> Corynebacterium glutamicum

<400> 88
 Ala Gln Arg Met Arg Ile Ser Phe Pro Arg His Gln Arg Gly Arg Phe
 1 5 10 15

Leu Cys Ile Ala Asp Phe Ile Arg Pro Arg Glu Gln Ala Val Lys Asp
 20 25 30

Gly Gln Val Asp Val Met Pro Phe Gln Leu Val Thr Met Gly Asn Pro
 35 40 45

Ile Ala Asp Phe Ala Asn Glu Leu Phe Ala Ala Asn Glu Tyr Arg Glu
 50 55 60

Tyr Leu Glu Val His Gly Ile Gly Val Gln Leu Thr Glu Ala Leu Ala
 65 70 75 80

Glu Tyr Trp His Ser Arg Val Arg Ser Glu Leu Lys Leu Asn Asp Gly
 85 90 95

Gly Ser Val Ala Asp Phe Asp Pro Glu Asp Lys Thr Lys Phe Phe Asp
 100 105 110

Leu Asp Tyr Arg Gly Ala Arg Phe Ser Phe Gly Tyr Gly Ser Cys Pro
 115 120 125

Asp Leu Glu Asp Arg Ala Lys Leu Val Glu Leu Leu Glu Pro Gly Arg
 130 135 140

Ile Gly Val Glu Leu Ser Glu Glu Leu Gln Leu His Pro Glu Gln Ser
 145 150 155 160

Thr Asp Ala Phe Val Leu Tyr His Pro Glu Ala Lys Tyr Phe Asn Val
 165 170 175

<210> 89

<211> 2599
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(2599)
 <223> RXN02198

<400> 89

agactagtgg cgttttgccg gtgttgctta ggaggcgttg aaaatgaact acgaatgaaa 60

agttcgggaa ttgtctaatc cgtactaagg tgtctacaca atg tct act tca gtt 115
 Met Ser Thr Ser Val
 1 5

act tca cca ggt cac aac aac gaa cat tcc ttc aaa ttt ttg cat ggg 163
 Thr Ser Pro Ala His Asn Asn Ala His Ser Ser Glu Phe Leu Asp Ala
 10 15 20

ttg gaa aac cat gtg ttg atc ggt gag ggc aac atg gag aac cag ttc 211
 Leu Ala Asn His Val Leu Ile Gly Asp Gly Ala Met Gly Thr Gln Leu
 25 30 35

aaa ggc ttt gat ctg gac gtg gaa aag gat ttc att gat ctg gag ggt 259
 Gln Gly Phe Asp Leu Asp Val Gln Lys Asp Phe Leu Asp Leu Ala Gly
 40 45 50

tgt aat gat att ctg aac gac aac cgt cct gat ttg ttg agt cag att 307
 Cys Asn Glu Ile Leu Asn Asp Thr Arg Pro Asp Val Leu Arg Gln Ile
 55 60 65

cac ggc ggt tat ttt gag gag gga ggt cac ttg gtt gag aac aat aat 355
 His Arg Ala Tyr Phe Gln Ala Gly Ala Asp Leu Val Glu Thr Asn Thr
 70 75 80 85

ttt ggt ttg aac ctg cgg aac ttg ggg gat tat gac atc got gat agt 403
 Phe Gly Cys Asn Leu Pro Asn Leu Ala Asp Tyr Asp Ile Ala Asp Arg
 90 95 100

tgc cgt gag ctt gcc tac aag ggc act gca gtg got agg gaa gtg got 451
 Cys Arg Glu Leu Ala Tyr Lys Gly Thr Ala Val Ala Arg Glu Val Ala
 105 110 115

gat gag atg ggg cgg ggc cga aac ggc atg cgg cgt ttc gtg gtt ggt 499
 Asp Glu Met Gly Pro Gly Arg Asn Gly Met Arg Arg Phe Val Val Gly
 120 125 130

tcc ctg gga cct gga acg aag ctt cca tcc ctg ggc cat gca cgg tat 547
 Ser Leu Gly Pro Gly Thr Lys Leu Pro Ser Leu Gly His Ala Pro Tyr
 135 140 145

gca gat ttg cgt ggg cac tac aag gaa gca ggc ctt ggc atc atc gac 595
 Ala Asp Leu Arg Gly His Tyr Lys Glu Ala Ala Leu Gly Ile Ile Asp
 150 155 160 165

ggg ggt ggc gat gcc ttt ttg att gag act got cag gac ttg ctt cag 643
 Gly Gly Gly Asp Ala Phe Leu Ile Glu Thr Ala Gln Asp Leu Leu Gln
 170 175 180

gtc aag got gag gtt cac ggc gtt caa gat gcc atg got gaa ttt gat 691

Val	Lys	Ala	Ala	Val	His	Gly	Val	Gln	Asp	Ala	Met	Ala	Glu	Leu	Asp		
			185					190					195				
aaa	ttc	ttg	ccc	att	att	tgc	cac	gtc	acc	gta	gag	acc	acc	ggc	acc	739	
Thr	Phe	Leu	Pro	Ile	Ile	Cys	His	Val	Thr	Val	Glu	Thr	Thr	Gly	Thr		
		200				205					210						
atg	ctc	atg	ggt	tct	gag	acc	ggg	ggt	gag	ttg	aaa	gag	ctg	cag	cca	787	
Met	Leu	Met	Gly	Ser	Glu	Ile	Gly	Ala	Ala	Leu	Thr	Ala	Leu	Gln	Pro		
	215				220					225							
ctg	ggg	atc	gac	atg	att	ggg	ctg	aac	tgc	gcc	acc	ggc	cca	gat	gag	835	
Leu	Gly	Ile	Asp	Met	Ile	Gly	Leu	Asn	Cys	Ala	Thr	Gly	Pro	Asp	Glu		
230				235				240						245			
atg	agg	gag	caa	ctg	ggt	tac	ctg	tcc	aag	caa	gac	gat	att	cct	gtg	883	
Met	Ser	Glu	His	Leu	Arg	Tyr	Leu	Ser	Lys	His	Ala	Asp	Ile	Pro	Val		
			250					255					260				
tgg	gtg	atg	cct	aac	gca	ggt	ctt	cct	ctc	ctg	ggg	aaa	aac	ggt	cca	931	
Ser	Val	Met	Pro	Asn	Ala	Gly	Leu	Pro	Val	Leu	Gly	Lys	Asn	Gly	Ala		
		265					270					275					
gaa	tac	cca	ctt	gag	ggt	gag	gat	ttg	gtg	cag	gag	ctg	tct	gaa	ttc	979	
Gln	Tyr	Pro	Leu	Glu	Ala	Gln	Asp	Leu	Ala	Gln	Ala	Leu	Ala	Gly	Ile		
	285					285						290					
gtc	tac	aaa	tac	ggc	ctg	tcc	atg	gtg	ggt	ggt	tgt	tgt	ggc	acc	aaa	1027	
Val	Ser	Glu	Tyr	Gly	Leu	Ser	Met	Val	Gly	Gly	Cys	Cys	Gly	Thr	Thr		
	295				300					305							
cct	gag	caa	atc	ggt	ggt	gtc	ggt	ggt	ggt	ggt	ggt	ggt	ggt	ggt	ggt	1075	
Pro	Glu	His	Ile	Arg	Ala	Val	Arg	Asp	Ala	Val	Val	Gly	Val	Pro	Glu		
310				315				320					325				
cag	gaa	acc	tcc	aaa	ctg	acc	aag	atc	cct	gca	ggc	cct	gtt	gag	cag	1123	
Gln	Glu	Thr	Ser	Thr	Leu	Thr	Lys	Ile	Pro	Ala	Gly	Pro	Val	Glu	Gln		
			330					335					340				
gcc	tcc	ggc	gag	gtg	gag	aaa	gag	gac	tcc	gtc	ggc	tgc	ctg	tac	acc	1171	
Ala	Ser	Arg	Glu	Val	Glu	Lys	Glu	Asp	Ser	Val	Ala	Ser	Leu	Tyr	Thr		
			345					350					355				
tgc	gtg	cca	ttg	tcc	cag	gaa	acc	ggc	att	tcc	atg	atc	ggg	gag	ggc	1219	
Ser	Val	Pro	Leu	Ser	Gln	Glu	Thr	Gly	Ile	Ser	Met	Ile	Gly	Glu	Arg		
		360					365					370					
acc	aac	tcc	aac	ggg	tcc	aag	gca	ttc	cgt	gag	gca	atg	ctg	tct	ggc	1267	
Thr	Asn	Ser	Asn	Gly	Ser	Lys	Ala	Phe	Arg	Glu	Ala	Met	Leu	Ser	Gly		
	375					380					385						
gat	tgg	gaa	aag	tgt	gtg	gat	att	gcc	aag	cag	caa	acc	ggc	gat	ggg	1315	
Asp	Trp	Glu	Lys	Cys	Val	Asp	Ile	Ala	Lys	Gln	Gln	Thr	Arg	Asp	Gly		
390				395				400					405				
gca	caa	atg	ctg	gat	ctt	tgt	gtg	gat	tac	gtg	gga	cga	gac	ggc	acc	1363	
Ala	His	Met	Leu	Asp	Leu	Cys	Val	Asp	Tyr	Val	Gly	Arg	Asp	Gly	Thr		
			410					415					420				
gcc	gat	atg	ggg	acc	ttg	gca	gca	ctt	ctt	ggt	acc	agg	tcc	act	ttg	1411	
Ala	Asp	Met	Ala	Thr	Leu	Ala	Ala	Leu	Leu	Ala	Thr	Ser	Ser	Thr	Leu		

425	430	435	
cca atc atg att gac tcc acc gag cca gag gtt att cgc aca ggc ctt	1459		
Pro Ile Met Ile Asp Ser Thr Glu Pro Glu Val Ile Arg Thr Gly Leu			
440	445	450	
gag cac ttg ggt gga cga agc atc gtt aac tcc gtc aac ttt gaa gac	1507		
Glu His Leu Gly Gly Arg Ser Ile Val Asn Ser Val Asn Phe Glu Asp			
455	460	465	
ggc gat ggc cct gag tcc cgc tac cag cgc atc atg aaa ctg gta aag	1555		
Gly Asp Gly Pro Glu Ser Arg Tyr Gln Arg Ile Met Lys Leu Val Lys			
470	475	480	485
cag cac ggt gag gcc gng gtt gcg ctg acc att gat gag gaa ggc cag	1603		
Gln His Gly Ala Ala Val Val Ala Leu Thr Ile Asp Glu Glu Gly Gln			
490	495	500	
gca cgt acc gct gag cac aag gtg cgc att gct aaa cga ctg att gac	1651		
Ala Arg Thr Ala Glu His Lys Val Arg Ile Ala Lys Arg Leu Ile Asp			
505	510	515	
gat atc aac ggt agc tac ggc ctg gat atc aaa gac atc gtt gtg gac	1699		
Asp Ile Thr Gly Ser Tyr Gly Leu Asp Ile Lys Asp Ile Val Val Asp			
520	525	530	
tgc ctg att ttt ctt atc tct act tgc ctg gaa gta att att cga gat	1747		
Cys Leu Thr Phe Pro Ile Ser Thr Gly Gln Gln Gln Thr Arg Arg Asp			
535	540	545	
ggc att gaa acc atc gaa gcc atc cgc gag ctg aag aag ctg tac cca	1795		
Gly Ile Glu Thr Ile Glu Ala Ile Arg Glu Leu Lys Lys Leu Tyr Pro			
550	555	560	565
gaa atc cac acc acc ctg ggt ctg tcc aat att tcc ttc ggc ctg aac	1843		
Glu Ile His Thr Thr Leu Gly Leu Ser Asn Ile Ser Phe Gly Leu Asn			
570	575	580	
cct gct gca cgc cag gtt ctt aac tct gtg ttc ctg aat gag tgc att	1891		
Pro Ala Ala Arg Gln Val Leu Asn Ser Val Phe Leu Asn Glu Cys Ile			
585	590	595	
gag gct ggt ctg gac tct gcg att gcg cac agc tcc aag att ttg ccg	1939		
Glu Ala Gly Leu Asp Ser Ala Ile Ala His Ser Ser Lys Ile Leu Pro			
600	605	610	
atg aac cgc att gat gat cgc cag cgc gaa gtg gcg ttg gat atg gtc	1987		
Met Asn Arg Ile Asp Asp Arg Gln Arg Glu Val Ala Leu Asp Met Val			
615	620	625	
tat gat cgc cgc acc gag gat tac gat ccg ctg cag gaa ttc atg cag	2035		
Tyr Asp Arg Arg Thr Glu Asp Tyr Asp Pro Leu Gln Glu Phe Met Gln			
630	635	640	645
ctg ttt gag ggc gtt tct gct gcc gat gcc aag gat gct cgc gct gaa	2083		
Leu Phe Glu Gly Val Ser Ala Ala Asp Ala Lys Asp Ala Arg Ala Glu			
650	655	660	
cag ctg gcc gct atg cct ttg ttt gag cgt ttg gaa cag cgc atc atc	2131		
Gln Leu Ala Ala Met Pro Leu Phe Glu Arg Leu Ala Gln Arg Ile Ile			
665	670	675	

gac ggc gat aag aat ggc ctt gag gat gat ctg gaa gca ggc atg aag 2179
 Asp Gly Asp Lys Asn Gly Leu Glu Asp Asp Leu Glu Ala Gly Met Lys
 680 685 690

gag aag tct cct att ggc atc atc aac gag gac ctt ctc aac ggc atg 2227
 Glu Lys Ser Pro Ile Ala Ile Ile Asn Glu Asp Leu Leu Asn Gly Met
 695 700 705

aag aac gtg ggt gag ctg ttt ggt tcc gga cag atg cag ctg gca ttc 2275
 Lys Thr Val Gly Glu Leu Phe Gly Ser Gly Gln Met Gln Leu Pro Phe
 710 715 720 725

gtg ctg caa tcg gca gaa acc atg aaa act gcg gtg gcc tat ttg gaa 2323
 Val Leu Gln Ser Ala Glu Thr Met Lys Thr Ala Val Ala Tyr Leu Glu
 730 735 740

ccg ttc atg gaa gag gaa gca gaa gat aac gga ttc tcc cag gaa gag 2371
 Pro Phe Met Glu Glu Glu Ala Glu Ala Thr Gly Ser Ala Gln Ala Glu
 745 750 755

ggc aag ggc aaa atc gtc gtg gcc aac gtc aag ggt gac gtc cag gat 2419
 Gly Lys Gly Lys Ile Val Val Ala Thr Val Lys Gly Asp Val His Asp
 760 765 770

ctc ggt aag aac ttc gtg gac atc att ttg ttc aac aac ggt ttc gac 2467
 Ile Gly Lys Asn Leu Val Asp Ile Ile Leu Ser Asn Asn Gly Tyr Asp
 775 780 785

gtg gtg aac ttg ggc atc aag cag gca ctg tcc gcc atg ttg gaa gca 2515
 Val Val Asn Leu Gly Ile Lys Gln Pro Leu Ser Ala Met Leu Glu Ala
 790 795 800 805

gag gaa gaa aac aac gca gac gtc atc ggc att ttg gga ttc att gtg 2563
 Ala Glu Glu His Lys Ala Asp Val Ile Gly Met Ser Gly Leu Leu Val
 810 815 820

aag tcc aac gtg gtg atg aag caa acc atc agc gac 2599
 Lys Ser Thr Val Val Met Lys Gln Thr Ile Ser Asp
 825 830

<210> 90

<211> 833

<212> PRT

<213> Corynebacterium glutamicum

<400> 90

Met Ser Thr Ser Val Thr Ser Pro Ala His Asn Asn Ala His Ser Ser
 1 5 10 15

Glu Phe Leu Asp Ala Leu Ala Asn His Val Leu Ile Gly Asp Gly Ala
 20 25 30

Met Gly Thr Gln Leu Gln Gly Phe Asp Leu Asp Val Glu Lys Asp Phe
 35 40 45

Leu Asp Leu Glu Gly Cys Asn Glu Ile Leu Asn Asp Thr Arg Pro Asp
 50 55 60

Val Leu Arg Gln Ile His Arg Ala Tyr Phe Glu Ala Gly Ala Asp Leu

65	70	75	80
Val Glu Thr Asn Thr Phe Gly Cys Asn Leu Pro Asn Leu Ala Asp Tyr	85	90	95
Asp Ile Ala Asp Arg Cys Arg Glu Leu Ala Tyr Lys Gly Thr Ala Val	100	105	110
Ala Arg Glu Val Ala Asp Glu Met Gly Pro Gly Arg Asn Gly Met Arg	115	120	125
Arg Phe Val Val Gly Ser Leu Gly Pro Gly Thr Lys Leu Pro Ser Leu	130	135	140
Gly His Ala Pro Tyr Ala Asp Leu Arg Gly His Tyr Lys Glu Ala Ala	145	150	155
Leu Gly Ile Ile Asp Gly Gly Gly Asp Ala Phe Leu Ile Glu Thr Ala	165	170	175
Gln Asp Leu Leu Gln Val Lys Ala Ala Val His Gly Val Gln Asp Ala	180	185	190
Met Ala Glu Leu Asp Thr Phe Leu Pro Ile Ile Cys His Val Thr Val	195	200	205
Glu Thr Thr Gly Thr Met Leu Met Gly Ser Glu Ile Gly Ala Ala Leu	210	215	220
Thr Ala Leu Gln Pro Leu Gly Ile Asp Met Ile Gly Leu Asn Cys Ala	225	230	235
Thr Gly Pro Asp Glu Met Ser Glu His Leu Arg Tyr Leu Ser Lys His	245	250	255
Ala Asp Ile Pro Val Ser Val Met Pro Asn Ala Gly Leu Pro Val Leu	260	265	270
Gly Lys Asn Gly Ala Glu Tyr Pro Leu Glu Ala Glu Asp Leu Ala Gln	275	280	285
Ala Leu Ala Gly Phe Val Ser Glu Tyr Gly Leu Ser Met Val Gly Gly	290	295	300
Cys Cys Gly Thr Thr Pro Glu His Ile Arg Ala Val Arg Asp Ala Val	305	310	315
Val Gly Val Pro Glu Gln Glu Thr Ser Thr Leu Thr Lys Ile Pro Ala	325	330	335
Gly Pro Val Glu Gln Ala Ser Arg Glu Val Glu Lys Glu Asp Ser Val	340	345	350
Ala Ser Leu Tyr Thr Ser Val Pro Leu Ser Gln Glu Thr Gly Ile Ser	355	360	365
Met Ile Gly Glu Arg Thr Asn Ser Asn Gly Ser Lys Ala Phe Arg Glu	370	375	380
Ala Met Leu Ser Gly Asp Trp Glu Lys Cys Val Asp Ile Ala Lys Gln	385	390	395
			400

Gln Thr Arg Asp Gly Ala His Met Leu Asp Leu Cys Val Asp Tyr Val
 405 410 415
 Gly Arg Asp Gly Thr Ala Asp Met Ala Thr Leu Ala Ala Leu Leu Ala
 420 425 430
 Thr Ser Ser Thr Leu Pro Ile Met Ile Asp Ser Thr Glu Pro Glu Val
 435 440 445
 Ile Arg Thr Gly Leu Glu His Leu Gly Gly Arg Ser Ile Val Asn Ser
 450 455 460
 Val Asn Phe Glu Asp Gly Asp Gly Pro Glu Ser Arg Tyr Gln Arg Ile
 465 470 475 480
 Met Lys Leu Val Lys Gln His Gly Ala Ala Val Val Ala Leu Thr Ile
 485 490 495
 Asp Glu Glu Gly Gln Ala Arg Thr Ala Glu His Lys Val Arg Ile Ala
 500 505 510
 Lys Arg Leu Ile Asp Asp Ile Thr Gly Ser Tyr Gly Leu Asp Ile Lys
 515 520 525
 Asp Ile Val Val Asp Cys Leu Thr Ile Pro Ile Ser Thr Gly Gln Gln
 530 535 540
 Glu Thr Arg Arg Asp Gly Ile Glu Thr Ile Glu Ala Ile Arg Glu Leu
 545 550 555 560
 Lys Lys Leu Tyr Pro Glu Ile His Thr Thr Leu Gly Leu Ser Asn Ile
 565 570 575
 Ser Phe Gly Leu Asn Pro Ala Ala Arg Gln Val Leu Asn Ser Val Phe
 580 585 590
 Leu Asn Glu Cys Ile Glu Ala Gly Leu Asp Ser Ala Ile Ala His Ser
 595 600 605
 Ser Lys Ile Leu Pro Met Asn Arg Ile Asp Asp Arg Gln Arg Glu Val
 610 615 620
 Ala Leu Asp Met Val Tyr Asp Arg Arg Thr Glu Asp Tyr Asp Pro Leu
 625 630 635 640
 Gln Glu Phe Met Gln Leu Phe Glu Gly Val Ser Ala Ala Asp Ala Lys
 645 650 655
 Asp Ala Arg Ala Glu Gln Leu Ala Ala Met Pro Leu Phe Glu Arg Leu
 660 665 670
 Ala Gln Arg Ile Ile Asp Gly Asp Lys Asn Gly Leu Glu Asp Asp Leu
 675 680 685
 Glu Ala Gly Met Lys Glu Lys Ser Pro Ile Ala Ile Ile Asn Glu Asp
 690 695 700
 Leu Leu Asn Gly Met Lys Thr Val Gly Glu Leu Phe Gly Ser Gly Gln
 705 710 715 720

Met Gln Leu Pro Phe Val Leu Gln Ser Ala Glu Thr Met Lys Thr Ala
 725 730 735

Val Ala Tyr Leu Glu Pro Phe Met Glu Glu Glu Ala Glu Ala Thr Gly
 740 745 750

Ser Ala Gln Ala Glu Gly Lys Gly Lys Ile Val Val Ala Thr Val Lys
 755 760 765

Gly Asp Val His Asp Ile Gly Lys Asn Leu Val Asp Ile Ile Leu Ser
 770 775 780

Asn Asn Gly Tyr Asp Val Val Asn Leu Gly Ile Lys Gln Pro Leu Ser
 785 790 795 800

Ala Met Leu Glu Ala Ala Glu Glu His Lys Ala Asp Val Ile Gly Met
 805 810 815

Ser Gly Leu Leu Val Lys Ser Thr Val Val Met Lys Gln Thr Ile Ser
 820 825 830

Asp

<210> 91
 <211> 2578
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(2578)
 <223> FRXA02198

<400> 91
 agactagtgg cgatttgcct gtgttgctta ggagggttg aaaatgaact acgaatgaaa 60
 agttcgggaa ttgtataatc cgtactaagg tgtctacaca atg tct act tca gtt 115
 Met Ser Thr Ser Val
 1 5

act tca cca gcc cac aac aac gca cat tcc tcc gaa ttt ttg gat ggc 163
 Thr Ser Pro Ala His Asn Asn Ala His Ser Ser Glu Phe Leu Asp Ala
 10 15 20

ttg gca aac cat gtg ttg atc ggc gac ggc gcc atg ggc acc cag ctc 211
 Leu Ala Asn His Val Leu Ile Gly Asp Gly Ala Met Gly Thr Gln Leu
 25 30 35

caa ggc ttt gac ctg gac gtg gaa aag gat ttc ctt gat ctg gag ggg 259
 Gln Gly Phe Asp Leu Asp Val Glu Lys Asp Phe Leu Asp Leu Glu Gly
 40 45 50

tgt aat gag att ctc aac gac acc cgc cct gat gtg ttg agg cag att 307
 Cys Asn Glu Ile Leu Asn Asp Thr Arg Pro Asp Val Leu Arg Gln Ile
 55 60 65

cac cgc gcc tac ttt gag ggc gga ggt gac ttg gtt gag att aat act 355
 His Arg Ala Tyr Phe Glu Ala Gly Ala Asp Leu Val Glu Thr Asn Thr
 70 75 80 85

ttt ggt tgc aac ctg ccg aac ttg ggg gat tat gac atc gct gat cgt	403
Phe Gly Cys Asn Leu Pro Asn Leu Ala Asp Tyr Asp Ile Ala Asp Arg	
90 95 100	
tgc cgt gag ctt gcc tac aag ggc act gca gtg gct agg gaa gtg gct	451
Cys Arg Glu Leu Ala Tyr Lys Gly Thr Ala Val Ala Arg Glu Val Ala	
105 110 115	
gat gag atg ggg ccg ggc cga aac ggc atg cgg cgt ttc gtg gtt ggt	499
Asp Glu Met Gly Pro Gly Arg Asn Gly Met Arg Arg Phe Val Val Gly	
120 125 130	
tcc ctg gga cct gga acg aag ctt cca tgg ctg ggc cat gca ccg tat	547
Ser Leu Gly Pro Gly Thr Lys Leu Pro Ser Leu Gly His Ala Pro Tyr	
135 140 145	
gca gat ttg cgt ggg cac tac aag gaa gca gag ctt ggc atc atc gac	595
Ala Asp Leu Arg Gly His Tyr Lys Glu Ala Ala Leu Gly Ile Ile Asp	
150 155 160 165	
ggt ggt agc gat ggc ttt tgg att gag act gct cag gac ttg att cag	643
Gly Gly Gly Asp Ala Phe Leu Ile Glu Thr Ala Gln Asp Leu Leu Gln	
170 175 180	
ttc aag cct ggg gtt cac agc gtt cca gat gcc att gct aac att gat	691
Val Lys Ala Ala Val His Gly Val Gln Asp Ala Met Ala Glu Leu Asp	
185 190 195	
aac ttc ttg ccc att att tgc cac gtc acc gta gag acc acc ggc acc	739
Thr Phe Leu Pro Ile Ile Cys His Val Thr Val Glu Thr Thr Gly Thr	
200 205 210	
atg ctc atg ggt cct gag atc ggt gcc ggg ttg aca ggg ctg cag cca	787
Met Leu Met Gly Ser Glu Ile Gly Ala Ala Leu Thr Ala Leu Gln Pro	
215 220 225	
ctg ggt atc gac atg att ggt ctg aac tgc gcc acc ggc cca gat gag	835
Leu Gly Ile Asp Met Ile Gly Leu Asn Cys Ala Thr Gly Pro Asp Glu	
230 235 240 245	
atg agc gag cac ctg cgt tac ctg tcc aag cac gcc gat att cct gtg	883
Met Ser Glu His Leu Arg Tyr Leu Ser Lys His Ala Asp Ile Pro Val	
250 255 260	
tgg gtg atg cct aac gca ggt ctt cct gtc ctg ggt aaa aac ggt gca	931
Ser Val Met Pro Asn Ala Gly Leu Pro Val Leu Gly Lys Asn Gly Ala	
265 270 275	
gaa tac cca ctt gag gct gag gat ttg ggg cag ggg ctg gct gga ttc	979
Glu Tyr Pro Leu Glu Ala Glu Asp Leu Ala Gln Ala Leu Ala Gly Phe	
280 285 290	
gtc tcc gaa tat ggc ctg tcc atg gtg ggt ggt tgt tgt ggc acc aca	1027
Val Ser Glu Tyr Gly Leu Ser Met Val Gly Gly Cys Cys Gly Thr Thr	
295 300 305	
cct gag cac atc cgt ggg gtc ccg gat ggg gtg gtt ggt gtt cca gag	1075
Pro Glu His Ile Arg Ala Val Arg Asp Ala Val Val Gly Val Pro Glu	
310 315 320 325	

cag gaa acc tcc aca ctg acc aag atc cct gca ggc cct gtt gag cag	1123
Gln Glu Thr Ser Thr Leu Thr Lys Ile Pro Ala Gly Pro Val Glu Gln	
330 335 340	
gac tcc cgc gag gtg gag aaa gag gac tcc gtc gcg tgg ctg tac acc	1171
Ala Ser Arg Glu Val Glu Lys Glu Asp Ser Val Ala Ser Leu Tyr Thr	
345 350 355	
tgg gtg cca ttg tcc cag gaa acc ggc att tcc atg atc ggt gag cgc	1219
Ser Val Pro Leu Ser Gln Glu Thr Gly Ile Ser Met Ile Gly Glu Arg	
360 365 370	
acc aac tcc aac ggt tcc aag gca ttc cgt gag gca atg cta tct ggc	1267
Thr Asn Ser Asn Gly Ser Lys Ala Phe Arg Glu Ala Met Leu Ser Gly	
375 380 385	
gat tgg gaa aag tgt gtg gat att gcc aag cag caa acc cgc gat ggt	1315
Asp Trp Glu Lys Cys Val Asp Ile Ala Lys Gln Gln Thr Arg Asp Gly	
390 395 400 405	
gca cac atg tgg ggt ctt tgg gtg gat taa gtg gga gga gac ggt aac	1363
Ala His Met Leu Asp Leu Cys Val Asp Tyr Val Gly Arg Asp Gly Thr	
410 415 420	
gcc gat atg gcg acc ttg gca gca ctt ctt gct acc agc tcc act ttg	1411
Ala Asp Met Ala Thr Leu Ala Ala Leu Leu Ala Thr Ser Ser Thr Leu	
425 430 435	
gca atc atg att gac tcc acc gag cca gac gtt att tgc aca ggc ctt	1459
Pro Ile Met Ile Asp Ser Thr Glu Pro Glu Val Ile Arg Thr Gly Leu	
440 445 450	
gag cac ttg ggt gga cga agc atc gtt aac tcc gtc aac ttt gaa gac	1507
Glu His Leu Gly Gly Arg Ser Ile Val Asn Ser Val Asn Phe Glu Asp	
455 460 465	
ggc gat ggc cct gag tcc cgc tac cag cgc atc atg aaa ctg gta aag	1555
Gly Asp Gly Pro Glu Ser Arg Tyr Gln Arg Ile Met Lys Leu Val Lys	
470 475 480 485	
cag cac ggt gcg gcc gtg gtt gcg ctg acc att gat gag gaa ggc cag	1603
Gln His Gly Ala Ala Val Val Ala Leu Thr Ile Asp Glu Glu Gly Gln	
490 495 500	
gca cgt acc gct gag cac aag gtg cgc att gct aaa cga ctg att gac	1651
Ala Arg Thr Ala Glu His Lys Val Arg Ile Ala Lys Arg Leu Ile Asp	
505 510 515	
gat atc acc ggc agc tac gcc ctg gat atc aaa gac atc gtt gtg gac	1699
Asp Ile Thr Gly Ser Tyr Gly Leu Asp Ile Lys Asp Ile Val Val Asp	
520 525 530	
tgc ctg acc ttc ccg atc tct act gcc cag gaa gaa acc agg cga gat	1747
Cys Leu Thr Phe Pro Ile Ser Thr Gly Gln Glu Glu Thr Arg Arg Asp	
535 540 545	
ggc att gaa acc atc gaa gcc atc cgc gag ctg aag aag ctc tac caa	1795
Gly Ile Glu Thr Ile Glu Ala Ile Arg Glu Leu Lys Lys Leu Tyr Pro	
550 555 560 565	
gaa atc cac acc acc ctg ggt ctg tcc aat att tcc ttc gcc ctg aac	1843

Glu Ile His Thr Thr Leu Gly Leu Ser Asn Ile Ser Phe Gly Leu Asn	
570	575 580
cct gct gca cgc cag gtt ctt aac tct gtg ttc ctc aat gag tgc att	1891
Pro Ala Ala Arg Gln Val Leu Asn Ser Val Phe Leu Asn Glu Cys Ile	
585	590 595
gag gct ggt ctg gac tct ggc att ggc cac agc tcc aag att ttg cgc	1939
Glu Ala Gly Leu Asp Ser Ala Ile Ala His Ser Ser Lys Ile Leu Pro	
600	605 610
atg aac cgc att gat gat cgc cag cgc gaa gtg ggc ttg gat atg gtc	1987
Met Asn Arg Ile Asp Asp Arg Gln Arg Glu Val Ala Leu Asp Met Val	
615	620 625
tat gat cgc cgc acc gag gat tac gat cgc ctg cag gaa ttc atg gag	2035
Tyr Asp Arg Arg Thr Glu Asp Tyr Asp Pro Leu Gln Glu Phe Met Gln	
630	635 640 645
ctg ttc gag ttc ggt tct gat gcc gat ggc aag gat gct ttc att gaa	2083
Leu Phe Glu Gly Val Ser Ala Ala Asp Ala Lys Asp Ala Arg Ala Glu	
650	655 660
gat ctg ggc att att ttc ttc gat cgt ttg gaa cag att att att	2131
Gln Leu Ala Ala Met Pro Leu Phe Glu Arg Leu Ala Gln Arg Ile Ile	
665	670 675
acc ggc gat arg aa' ggc ctt gag gat gat ttg gaa gca ggc att aag	2179
Asp Gly Asp Lys Asn Gly Leu Glu Asp Asp Leu Glu Ala Gly Met Lys	
680	685 690
gag aag tct cct att ggc atc atc aac gag gac ctt ctc aac ggc atg	2227
Glu Lys Ser Pro Ile Ala Ile Ile Asn Glu Asp Leu Leu Asn Gly Met	
695	700 705
aag acc gtg ggt gag ctg ttt ggt tcc gga cag atg cag ctg cca ttc	2275
Lys Thr Val Gly Glu Leu Phe Gly Ser Gly Gln Met Gln Leu Pro Phe	
710	715 720 725
gtg ctg caa tgc gca gaa acc atg aaa act gcg gtg gcc tat ttg gaa	2323
Val Leu Gln Ser Ala Glu Thr Met Lys Thr Ala Val Ala Tyr Leu Glu	
730	735 740
cgc ttc atg gaa gag gaa gca gaa gct acc gga tct gcg cag gca gag	2371
Pro Phe Met Glu Glu Glu Ala Glu Ala Thr Gly Ser Ala Gln Ala Glu	
745	750 755
ggc aag ggc aaa atc gtc gtg gcc acc gtc aag ggt gac gtg cac gat	2419
Gly Lys Gly Lys Ile Val Val Ala Thr Val Lys Gly Asp Val His Asp	
760	765 770
atc ggc aag aac ttg gtg gac atc att ttg tcc aac aac ggt tac gac	2467
Ile Gly Lys Asn Leu Val Asp Ile Ile Leu Ser Asn Asn Gly Tyr Asp	
775	780 785
gtg gtg aac ttg ggc atc aag cag cca ctg tcc gcc atg ttg gaa gca	2515
Val Val Asn Leu Gly Ile Lys Gln Pro Leu Ser Ala Met Leu Glu Ala	
790	795 800 805
gcg gaa gaa cac aaa gca gac gtc atc ggc atg tcc gga ctt ctt gtg	2563
Ala Glu Glu His Lys Ala Asp Val Ile Gly Met Ser Gly Leu Leu Val	

810

815

820

aag tcc acc gtg gtg
Lys Ser Thr Val Val
925

2578

<210> 92
<211> 826
<212> PRT
<213> Corynebacterium glutamicum

<400> 92
Met Ser Thr Ser Val Thr Ser Pro Ala His Asn Asn Ala His Ser Ser
1 5 10 15
Glu Phe Leu Asp Ala Leu Ala Asn His Val Leu Ile Gly Asp Gly Ala
20 25 30
Met Gly Thr Gln Leu Gln Gly Phe Asp Leu Asp Val Glu Lys Asp Phe
35 40 45
Leu Asp Leu Ala Gly Cys Asn Glu Ile Leu Asn Asp Thr Arg Pro Asp
50 55 60
Val Leu Arg Gln Ile His Arg Ala Tyr Phe Glu Ala Gly Ala Asp Leu
65 70 75
Val Glu Thr Asn Thr Phe Gly Cys Asn Leu Pro Asn Leu Ala Asp Tyr
85 90 95
Asp Ile Ala Asp Arg Cys Arg Glu Leu Ala Tyr Lys Gly Thr Ala Val
100 105 110
Ala Arg Glu Val Ala Asp Glu Met Gly Pro Gly Arg Asn Gly Met Arg
115 120 125
Arg Phe Val Val Gly Ser Leu Gly Pro Gly Thr Lys Leu Pro Ser Leu
130 135 140
Gly His Ala Pro Tyr Ala Asp Leu Arg Gly His Tyr Lys Glu Ala Ala
145 150 155 160
Leu Gly Ile Ile Asp Gly Gly Gly Asp Ala Phe Leu Ile Glu Thr Ala
165 170 175
Gln Asp Leu Leu Gln Val Lys Ala Ala Val His Gly Val Gln Asp Ala
180 185 190
Met Ala Glu Leu Asp Thr Phe Leu Pro Ile Ile Cys His Val Thr Val
195 200 205
Glu Thr Thr Gly Thr Met Leu Met Gly Ser Glu Ile Gly Ala Ala Leu
210 215 220
Thr Ala Leu Gln Pro Leu Gly Ile Asp Met Ile Gly Leu Asn Cys Ala
225 230 235 240
Thr Gly Pro Asp Glu Met Ser Glu His Leu Arg Tyr Leu Ser Lys His
245 250 255

Ala Asp Ile Pro Val Ser Val Met Pro Asn Ala Gly Leu Pro Val Leu
 260 265 270
 Gly Lys Asn Gly Ala Glu Tyr Pro Leu Glu Ala Glu Asp Leu Ala Gln
 275 280 285
 Ala Leu Ala Gly Phe Val Ser Glu Tyr Gly Leu Ser Met Val Gly Gly
 290 295 300
 Cys Cys Gly Thr Thr Pro Glu His Ile Arg Ala Val Arg Asp Ala Val
 305 310 315 320
 Val Gly Val Pro Glu Gln Glu Thr Ser Thr Leu Thr Lys Ile Pro Ala
 325 330 335
 Gly Pro Val Glu Gln Ala Ser Arg Glu Val Glu Lys Glu Asp Ser Val
 340 345 350
 Ala Ser Leu Tyr Thr Ser Val Pro Leu Ser Gln Glu Thr Gly Ile Ser
 355 360 365
 Met Ile Gly Glu Arg Thr Asn Ser Asn Gly Ser Lys Ala Phe Arg Glu
 370 375 380
 Ala Met Leu Ser Gly Asp Trp Glu Lys Cys Val Asp Ile Ala Lys Gln
 385 390 395 400
 Gln Thr Arg Asp Gly Ala His Met Leu Asp Leu Cys Val Asp Tyr Val
 405 410 415
 Gly Arg Asp Gly Thr Ala Asp Met Ala Thr Leu Ala Ala Leu Leu Ala
 420 425 430
 Thr Ser Ser Thr Leu Pro Ile Met Ile Asp Ser Thr Glu Pro Glu Val
 435 440 445
 Ile Arg Thr Gly Leu Glu His Leu Gly Gly Arg Ser Ile Val Asn Ser
 450 455 460
 Val Asn Phe Glu Asp Gly Asp Gly Pro Glu Ser Arg Tyr Gln Arg Ile
 465 470 475 480
 Met Lys Leu Val Lys Gln His Gly Ala Ala Val Val Ala Leu Thr Ile
 485 490 495
 Asp Glu Glu Gly Gln Ala Arg Thr Ala Glu His Lys Val Arg Ile Ala
 500 505 510
 Lys Arg Leu Ile Asp Asp Ile Thr Gly Ser Tyr Gly Leu Asp Ile Lys
 515 520 525
 Asp Ile Val Val Asp Cys Leu Thr Phe Pro Ile Ser Thr Gly Gln Glu
 530 535 540
 Glu Thr Arg Arg Asp Gly Ile Glu Thr Ile Glu Ala Ile Arg Glu Leu
 545 550 555 560
 Lys Lys Leu Tyr Pro Glu Ile His Thr Thr Leu Gly Leu Ser Asn Ile
 565 570 575
 Ser Phe Gly Leu Asn Pro Ala Ala Arg Gln Val Leu Asn Ser Val Phe

580

585

590

Leu Asn Glu Cys Ile Glu Ala Gly Leu Asp Ser Ala Ile Ala His Ser
595 600 605

Ser Lys Ile Leu Pro Met Asn Arg Ile Asp Asp Arg Gln Arg Glu Val
610 615 620

Ala Leu Asp Met Val Tyr Asp Arg Arg Thr Glu Asp Tyr Asp Pro Leu
625 630 635 640

Gln Glu Phe Met Gln Leu Phe Glu Gly Val Ser Ala Ala Asp Ala Lys
645 650 655

Asp Ala Arg Ala Glu Gln Leu Ala Ala Met Pro Leu Phe Glu Arg Leu
660 665 670

Ala Gln Arg Ile Ile Asp Gly Asp Lys Asn Gly Leu Glu Asp Asp Leu
675 680 685

Glu Ala Gly Met Lys Glu Lys Ser Pro Ile Ala Ile Ile Asn Glu Asp
690 695 700

Leu Leu Asn Gly Met Lys Thr Val Gly Glu Leu Phe Gly Ser Gly Gln
705 710 715 720

Met Gln Leu Pro Phe Val Leu Gln Ser Ala Glu Thr Met Lys Thr Ala
725 730 735

Val Ala Tyr Leu Glu Pro Phe Met Glu Glu Glu Ala Glu Ala Thr Gly
740 745 750

Ser Ala Gln Ala Glu Gly Lys Gly Lys Ile Val Val Ala Thr Val Lys
755 760 765

Gly Asp Val His Asp Ile Gly Lys Asn Leu Val Asp Ile Ile Leu Ser
770 775 780

Asn Asn Gly Tyr Asp Val Val Asn Leu Gly Ile Lys Gln Pro Leu Ser
785 790 795 800

Ala Met Leu Glu Ala Ala Glu Glu His Lys Ala Asp Val Ile Gly Met
805 810 815

Ser Gly Leu Leu Val Lys Ser Thr Val Val
820 825

<100> 33

<110> 621

<120> DNA

<130> Corynebacterium glutamicum

<140>

<150> CDS

<160> (101)...(598)

<210> EXN03074

<400> 33

tttgtgggca atctgtttt ttctgaattg tgtgggatga atctcttaaa aattcacatt 60

tagcaggaca agcatactgt tttagttcta tgcctgtgggc atg act caa agt get 115
Met Thr Gln Ser Ala
1 5

cca gaa ttc att gcc acc gca gac ctg gta gac atc atc ggc gac aac 163
Pro Glu Phe Ile Ala Thr Ala Asp Leu Val Asp Ile Ile Gly Asp Asn
10 15 20

ggg caa tca tgc gac act cag ttt caa aac ctt gga ggt gcc aca gaa 211
Ala Gln Ser Cys Asp Thr Gln Phe Gln Asn Leu Gly Gly Ala Thr Glu
25 30 35

ttc cac gga ata ata acc acc gtg aat tgc ttc caa gac aac gcc ctg 259
Phe His Gly Ile Ile Thr Thr Val Lys Cys Phe Gln Asp Asn Ala Leu
40 45 50

ctg aaa tcc atc ctg agc gag gat aat cct ggg gga gtg ctg gtt atc 307
Leu Lys Ser Ile Leu Ser Glu Asp Asn Pro Gly Gly Val Leu Val Ile
55 60 65

gat ggc gac gca ttc gtg cac aac ggt cta gtt gga gac atc att gaa 355
Asp Gly Asp Ala Ser Val His Thr Ala Leu Val Gly Asp Ile Ile Ala
70 75 80 85

gga ctt gga aaa gat cat ggt tgg tcc gga gta att gtc aac gga gca 403
Gly Leu Gly Lys Asp His Gly Trp Ser Gly Val Ile Val Asn Gly Ala
90 95 100

att gga gat ttc gca atc atc ggc aat atc acc ttt ggt tgt aaa ggt 451
Ile Arg Asp Ser Ala Val Ile Gly Thr Met Thr Phe Gly Cys Lys Ala
105 110 115

ctt gga acc aac ccg cgg aaa tcc act aaa act ggt tcc ggc gaa cga 499
Leu Gly Thr Asn Pro Arg Lys Ser Thr Lys Thr Gly Ser Gly Glu Arg
120 125 130

gac gta gta gta tgc att ggt ggc att gac ttc att cct ggt cat tac 547
Asp Val Val Val Ser Ile Gly Gly Ile Asp Phe Ile Pro Gly His Tyr
135 140 145

gtc tac ggc gac tct gac gga att atc gtc acc gag gcg cca att aag 595
Val Tyr Ala Asp Ser Asp Gly Ile Ile Val Thr Glu Ala Pro Ile Lys
150 155 160 165

cag taatttggtt tgaacgacgca gta 621
Gln

<210> 94
<211> 166
<212> PRT
<213> Corynebacterium glutamicum

<400> 94
Met Thr Gln Ser Ala Pro Glu Phe Ile Ala Thr Ala Asp Leu Val Asp
1 5 10 15
Ile Ile Gly Asp Asn Ala Gln Ser Cys Asp Thr Gln Phe Gln Asn Leu
20 25 30

Gly Gly Ala Thr Glu Phe His Gly Ile Ile Thr Thr Val Lys Cys Phe
 35 40 45

Gln Asp Asn Ala Leu Leu Lys Ser Ile Leu Ser Glu Asp Asn Pro Gly
 50 55 60

Gly Val Leu Val Ile Asp Gly Asp Ala Ser Val His Thr Ala Leu Val
 65 70 75 80

Gly Asp Ile Ile Ala Gly Leu Gly Lys Asp His Gly Trp Ser Gly Val
 85 90 95

Ile Val Asn Gly Ala Ile Arg Asp Ser Ala Val Ile Gly Thr Met Thr
 100 105 110

Phe Gly Cys Lys Ala Leu Gly Thr Asn Pro Arg Lys Ser Thr Lys Thr
 115 120 125

Gly Ser Gly Glu Arg Asp Val Val Val Ser Ile Gly Gly Ile Asp Phe
 130 135 140

Ile Pro Gly His Tyr Val Tyr Ala Asp Ser Asp Gly Ile Ile Val Thr
 145 150 155 160

Glu Ala Pro Ile Lys Gln
 165

<210> 95
 <211> 621
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> [101]..(538)
 <223> FRXA02906

<400> 95
 ttgtgtgggca atgtgtgttt ttgttaattg tgtgggatga atgtttttaaa aatttcacatt 60
 tagcaggaca agcataactgt tttagtgtta tgtgtgtggc atg act caa agt got 115
 Met Thr Gln Ser Ala
 1 5

caa gaa ttc att gcc acc gca gac ctg gta gac atc atc ggc gac aac 163
 Pro Glu Phe Ile Ala Thr Ala Asp Leu Val Asp Ile Ile Gly Asp Asn
 10 15 20

ggc caa tca tgc gac act cag ttt caa aac ctt gga ggt gcc aca gaa 211
 Ala Gln Ser Cys Asp Thr Gln Phe Gln Asn Leu Gly Gly Ala Thr Glu
 25 30 35

ttc cac gga ata ata acc acc gtg aaa tgc ttc caa gac aac gcc ctg 259
 Phe His Gly Ile Ile Thr Thr Val Lys Cys Phe Gln Asp Asn Ala Leu
 40 45 50

ctg aaa tcc atc ctg agc gag gat aat cct ggg gga gtc ctg gtt atc 307
 Leu Lys Ser Ile Leu Ser Glu Asp Asn Pro Gly Gly Val Leu Val Ile
 55 60 65

gat ggc gac gea tcc gtg cac aac ggc cta gtt ggc gac atc att gea 355
 Asp Gly Asp Ala Ser Val His Thr Ala Leu Val Gly Asp Ile Ile Ala
 70 75 80 85

gga ctt gga aaa gat cat ggt tgg tcc gga gta att gtc aac gga gea 403
 Gly Leu Gly Lys Asp His Gly Trp Ser Gly Val Ile Val Asn Gly Ala
 90 95 100

att cga gac tcc gea gtc atc ggc aac atg acc ttt ggt tgt aaa ggc 451
 Ile Arg Asp Ser Ala Val Ile Gly Thr Met Thr Phe Gly Cys Lys Ala
 105 110 115

ctt gga acc aac cgg cgg aaa tcc act aaa act ggt tcc ggc gaa cga 499
 Leu Gly Thr Asn Pro Arg Lys Ser Thr Lys Thr Gly Ser Gly Glu Arg
 120 125 130

gac gta gtg gta tcc att ggt ggc att gac ttc att cct ggt cat tac 547
 Asp Val Val Val Ser Ile Gly Gly Ile Asp Phe Ile Pro Gly His Tyr
 135 140 145

tta tcc gta gac tat gac gga att att gta aac gac tgg cga att aag 595
 Val Tyr Ala Asp Ser Asp Gly Ile Ile Val Thr Glu Ala Pro Ile Lys
 150 155 160 165

cag taatttggtt tgaaggacga gta 621
 Gln

<210> 96

<211> 160

<212> FRT

<213> Corynebacterium glutamicum

<400> 96

Met Thr Gln Ser Ala Pro Glu Phe Ile Ala Thr Ala Asp Leu Val Asp
 1 5 10 15

Ile Ile Gly Asp Asn Ala Gln Ser Cys Asp Thr Gln Phe Gln Asn Leu
 20 25 30

Gly Gly Ala Thr Glu Phe His Gly Ile Ile Thr Thr Val Lys Cys Phe
 35 40 45

Gln Asp Asn Ala Leu Leu Lys Ser Ile Leu Ser Glu Asp Asn Pro Gly
 50 55 60

Gly Val Leu Val Ile Asp Gly Asp Ala Ser Val His Thr Ala Leu Val
 65 70 75 80

Gly Asp Ile Ile Ala Gly Leu Gly Lys Asp His Gly Trp Ser Gly Val
 85 90 95

Ile Val Asn Gly Ala Ile Arg Asp Ser Ala Val Ile Gly Thr Met Thr
 100 105 110

Phe Gly Cys Lys Ala Leu Gly Thr Asn Pro Arg Lys Ser Thr Lys Thr
 115 120 125

Gly Ser Gly Glu Arg Asp Val Val Val Ser Ile Gly Gly Ile Asp Phe
 130 135 140

aac atg atc ctc gac gac ggc ggt gac gcc acc atg gct gtt att cgc 547
 Asn Met Ile Leu Asp Asp Gly Gly Asp Ala Thr Met Ala Val Ile Arg
 135 140 145

ggt cgc gaa tac gag cag gct ggt ctg gtt cca cca gca gag gcc aac	595
Gly Arg Glu Tyr Glu Gln Ala Gly Leu Val Pro Pro Ala Glu Ala Asn	
150 155 160 165	
gat tcc gat gag tac atc gca ttc ttg ggc atg ctg cgt gag gtt ctt	643
Asp Ser Asp Glu Tyr Ile Ala Phe Leu Gly Met Leu Arg Glu Val Leu	
170 175 180	
gct gca gag cct ggc aag tgg ggc aag atc gct gag gcc gtt aag ggt	691
Ala Ala Glu Pro Gly Lys Trp Gly Lys Ile Ala Glu Ala Val Lys Gly	
185 190 195	
gtc acc gag gaa acc acc acc ggt gtg cac cgc ctg tac cac ttc gct	739
Val Thr Glu Glu Thr Thr Thr Gly Val His Arg Leu Tyr His Phe Ala	
200 205 210	
gaa gaa ggt ggt ctg cct ttc cca gag atg aac gtc aac gac gct gtc	787
Glu Glu Cys Val Leu Pro Phe Pro Ala Met Asn Val Asn Asp Ala Val	
215 220 225	
atc aag ttc aat ttt gat aat aag tac ttt acc cgt cac tcc ctg atc	835
Thr Lys Ser Lys Phe Asp Asn Lys Tyr Gly Thr Arg His Ser Leu Ile	
230 235 240 245	
gac ggc aat aat ttt gat aat gac atc ctg aag ggt ggc aac aac gtc	883
Asp Gly Ile Asn Arg Ala Thr Asp Met Leu Met Gly Gly Lys Asn Val	
250 255 260	
ctt ttc ttt ttt tac ttc gat ttc ggt aat ggt tcc ttt gag gtt ttc	931
Leu Val Cys Gly Tyr Gly Asp Val Gly Lys Gly Cys Ala Glu Ala Phe	
265 270 275	
acc ggt ttt ggt ttt ttt ggt gtc aag ttc acc gaa gct gac cca atc aac	979
Asp Gly Gln Gly Ala Arg Val Lys Val Thr Glu Ala Asp Pro Ile Asn	
280 285 290	
gct ctt gag gat ctg atg gat ggc tac tct gtc gtc acc gtt gat gag	1027
Ala Leu Gln Ala Leu Met Asp Gly Tyr Ser Val Val Thr Val Asp Glu	
295 300 305	
gcc atc gag gac gcc gac atc gtg atc acc ggc acc ggc aac aag gac	1075
Ala Ile Glu Asp Ala Asp Ile Val Ile Thr Ala Thr Gly Asn Lys Asp	
310 315 320 325	
atc att tcc ttc gag cag atg ctg aag atg aag gat cac gct ctg ctg	1123
Ile Ile Ser Phe Glu Gln Met Leu Lys Met Lys Asp His Ala Leu Leu	
330 335 340	
ggc aac atc ggt cac ttt gat aat gag atc gat atg cat tcc ctg ttg	1171
Gly Asn Ile Gly His Phe Asp Asn Glu Ile Asp Met His Ser Leu Leu	
345 350 355	
cac cgc gac gac gtc acc cgc acc acg atc aag cca cag gtc gac gag	1219
His Arg Asp Asp Val Thr Arg Thr Thr Ile Lys Pro Gln Val Asp Glu	
360 365 370	
ttc acc ttc tcc acc ggt cgc tcc atc atc gtc ctg tcc gaa ggt cgc	1267
Phe Thr Phe Ser Thr Gly Arg Ser Ile Ile Val Leu Ser Glu Gly Arg	
375 380 385	
ctg ttg aat ctt ggc aat gcc acc gga cac cca tca ttt gtc atg tcc	1315

Leu Leu Asn Leu Gly Asn Ala Thr Gly His Pro Ser Phe Val Met Ser
 390 395 400 405
 aac tct ttc gcc gat cag acc att gcg cag atc gaa ctg ttc caa aac 1363
 Asn Ser Phe Ala Asp Gln Thr Ile Ala Gln Ile Glu Leu Phe Gln Asn
 410 415 420
 gaa gga cag tac gag aac gag gtc tac cgt ctg cct aag gtt ctc gac 1411
 Glu Gly Gln Tyr Glu Asn Glu Val Tyr Arg Leu Pro Lys Val Leu Asp
 425 430 435
 gaa aag gtg gca cgc atc cac gtt gag gct ctc ggt ggt cag ctc acc 1459
 Glu Lys Val Ala Arg Ile His Val Glu Ala Leu Gly Gly Gln Leu Thr
 440 445 450
 gaa ctg acc aag gag cag gct gag tac atc ggc gtt gac gtt gca ggc 1507
 Glu Leu Thr Lys Glu Gln Ala Glu Tyr Ile Gly Val Asp Val Ala Gly
 455 460 465
 cca ttc aag ccg gag cac tac cgc tac taatgattg taagattgag gga 1557
 Pro Phe Lys Pro Glu His Tyr Arg Tyr
 470 475
 <210> 94
 <211> 478
 <212> PRT
 <213> Corynebacterium glutamicum
 <400> 98
 Met Ala Gln Val Met Asp Phe Lys Val Ala Asp Leu Ser Leu Ala Glu
 1 10 15
 Ala Gly Arg His Gln Ile Arg Leu Ala Glu Tyr Glu Met Pro Gly Leu
 20 25 30
 Met Gln Leu Arg Lys Glu Phe Ala Asp Glu Gln Pro Leu Lys Gly Ala
 35 40 45
 Arg Ile Ala Gly Ser Ile His Met Thr Val Gln Thr Ala Val Leu Ile
 50 55 60
 Glu Thr Leu Thr Ala Leu Gly Ala Glu Val Arg Trp Ala Ser Cys Asn
 65 70 75 80
 Ile Phe Ser Thr Gln Asp Glu Ala Ala Ala Ile Val Val Gly Ser
 85 90 95
 Gly Thr Val Glu Glu Pro Ala Gly Val Pro Val Phe Ala Trp Lys Gly
 100 105 110
 Glu Ser Leu Glu Glu Tyr Trp Trp Cys Ile Asn Gln Ile Phe Ser Trp
 115 120 125
 Gly Asp Glu Leu Pro Asn Met Ile Leu Asp Asp Gly Gly Asp Ala Thr
 130 135 140
 Met Ala Val Ile Arg Gly Arg Glu Tyr Glu Gln Ala Gly Leu Val Pro
 145 150 155 160
 Pro Ala Glu Ala Asn Asp Ser Asp Glu Tyr Ile Ala Phe Leu Gly Met

165	170	175
Leu Arg Glu Val Leu Ala Ala Glu Pro Gly Lys Trp Gly Lys Ile Ala 180 185 190		
Glu Ala Val Lys Gly Val Thr Glu Glu Thr Thr Thr Gly Val His Arg 195 200 205		
Leu Tyr His Phe Ala Glu Glu Gly Val Leu Pro Phe Pro Ala Met Asn 210 215 220		
Val Asn Asp Ala Val Thr Lys Ser Lys Phe Asp Asn Lys Tyr Gly Thr 225 230 235 240		
Arg His Ser Leu Ile Asp Gly Ile Asn Arg Ala Thr Asp Met Leu Met 245 250 255		
Gly Gly Lys Asn Val Leu Val Cys Gly Tyr Gly Asp Val Gly Lys Gly 260 265 270		
Cys Ala Glu Ala Phe Asp Gly Gln Gly Ala Arg Val Lys Val Thr Glu 275 280 285		
Ala Asp Pro Ile Asn Ala Leu Gln Ala Leu Met Asp Gly Tyr Ser Val 290 295 300		
Val Thr Val Asp Glu Ala Ile Glu Asp Ala Asp Ile Val Ile Thr Ala 305 310 315 320		
Thr Gly Asn Lys Asp Ile Ile Ser Phe Glu Gln Met Leu Lys Met Lys 325 330 335		
Asp His Ala Leu Leu Gly Asn Ile Gly His Phe Asp Asn Glu Ile Asp 340 345 350		
Met His Ser Leu Leu His Arg Asp Asp Val Thr Arg Thr Thr Ile Lys 355 360 365		
Pro Gln Val Asp Glu Phe Thr Phe Ser Thr Gly Arg Ser Ile Ile Val 370 375 380		
Leu Ser Glu Gly Arg Leu Leu Asn Leu Gly Asn Ala Thr Gly His Pro 385 390 395 400		
Ser Phe Val Met Ser Asn Ser Phe Ala Asp Gln Thr Ile Ala Gln Ile 405 410 415		
Glu Leu Phe Gln Asn Glu Gly Gln Tyr Glu Asn Glu Val Tyr Arg Leu 420 425 430		
Pro Lys Val Leu Asp Glu Lys Val Ala Arg Ile His Val Glu Ala Leu 435 440 445		
Gly Gly Gln Leu Thr Glu Leu Thr Lys Glu Gln Ala Glu Tyr Ile Gly 450 455 460		
Val Asp Val Ala Gly Pro Phe Lys Pro Glu His Tyr Arg Tyr 465 470 475		

<211> 128
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (1)..(105)
 <223> FRXA00132

<400> 98
 cac att gag gat ctc ggc ggt cag ctc aac gaa atg aac aag gag cag 48
 His Val Glu Ala Leu Gly Gly Gln Leu Thr Glu Leu Thr Lys Glu Gln
 1 5 10 15
 gtt cag tac atc ggc ggt gac gtt gaa ggc cca ttc aag cag gag cag 96
 Ala Glu Tyr Ile Gly Val Asp Val Ala Gly Pro Phe Lys Pro Glu His
 20 25 30
 tac cgc tac taatgattgt cagcattgag gga 128
 Tyr Arg Tyr
 35

<210> 100
 <211> 35
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 100
 His Val Glu Ala Leu Gly Gly Gln Leu Thr Glu Leu Thr Lys Glu Gln
 1 5 10 15
 Ala Glu Tyr Ile Gly Val Asp Val Ala Gly Pro Phe Lys Pro Glu His
 20 25 30
 Tyr Arg Tyr
 35

<210> 101
 <211> 1396
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1396)
 <223> FRXA01371

<400> 101
 aacagattca atcaattcgg tgtccactcc aacatgtaga gtggtgcgcg ttaaaaaagt 60
 ttctctaatt ttcatcttct taaaaggagg tcgcacaggac atg gca cag gtt atg 115
 Met Ala Gln Val Met
 1 5
 gac ttc aag gtt gcc gat ctt tca cta gca gag gca gga cgt cac cag 163
 Asp Phe Lys Val Ala Asp Leu Ser Leu Ala Glu Ala Gly Arg His Gln
 10 15 20
 att cgt ctt gca gag tat gag atg cca ggt ctc atg cag ttg cgc aag 211

Ile	Arg	Leu	Ala	Glu	Tyr	Glu	Met	Pro	Gly	Leu	Met	Gln	Leu	Arg	Lys		
			25					30					35				
gaa	ttc	gca	gac	gag	cag	cct	ttg	aag	ggc	gcc	cga	att	gct	ggg	tct	259	
Glu	Phe	Ala	Asp	Glu	Gln	Pro	Leu	Lys	Gly	Ala	Arg	Ile	Ala	Gly	Ser		
		40					45					50					
atc	cat	atg	aag	gtc	cag	acc	gcc	gtg	ctt	att	gag	acc	ctc	aac	gct	307	
Ile	His	Met	Thr	Val	Gln	Thr	Ala	Val	Leu	Ile	Glu	Thr	Leu	Thr	Ala		
	55					60					65						
ttg	ggc	gct	gag	gtt	cct	tgg	gct	tcc	tgc	aac	att	ttc	tcc	acc	cag	355	
Leu	Gly	Ala	Glu	Val	Arg	Trp	Ala	Ser	Cys	Asn	Ile	Phe	Ser	Thr	Gln		
	70				75				80					85			
gat	jag	gat	gca	ggg	gct	atc	gtt	gtc	ggc	tcc	ggc	aac	gtc	gaa	gag	403	
Asp	Glu	Ala	Ala	Ala	Ile	Val	Val	Gly	Ser	Gly	Thr	Val	Glu	Glu			
			90					95					100				
cca	gat	gat	ggt	cca	ala	tta	ggg	tgg	aag	ggt	gag	tta	tta	gag	gag	451	
Pro	Ala	Gly	Val	Pro	Val	Phe	Ala	Trp	Lys	Gly	Glu	Ser	Leu	Glu	Glu		
		105						110					115				
tac	tgg	tgg	tgc	atc	aac	cag	atc	tta	arg	tgg	ggc	gat	gat	atg	cca	499	
Tyr	Trp	Trp	Cys	Ile	Asn	Gln	Ile	Phe	Ser	Trp	Gly	Asp	Glu	Leu	Pro		
	120					125						130					
aac	att	att	tta	gac	gac	ggc	ggg	gat	gtt	aac	atg	gat	gtt	att	agg	547	
Asn	Met	Ile	Leu	Asp	Asp	Gly	Gly	Asp	Ala	Thr	Met	Ala	Val	Ile	Arg		
	135					140					145						
ggg	gat	gaa	tac	gag	cag	gct	ggg	cag	gtt	cca	cca	gaa	gag	gtc	aac	595	
Gly	Arg	Glu	Tyr	Glu	Gln	Ala	Gly	Leu	Val	Pro	Pro	Ala	Glu	Ala	Asn		
	150				155					160					165		
gat	tac	gat	gag	tac	atc	gca	tta	tta	ggc	atg	ctg	cgt	gag	gtt	ctt	643	
Asp	Ser	Asp	Glu	Tyr	Ile	Ala	Phe	Leu	Gly	Met	Leu	Arg	Glu	Val	Leu		
			170						175					180			
gct	gca	gag	cct	ggc	aag	tgg	ggc	aag	atc	gct	gag	gcc	gtt	aag	ggg	691	
Ala	Ala	Glu	Pro	Gly	Lys	Trp	Gly	Lys	Ile	Ala	Glu	Ala	Val	Lys	Gly		
		185						190					195				
gtc	acc	gag	gaa	acc	acc	acc	ggg	gtg	cac	cgc	ctg	tac	cac	tta	gct	739	
Val	Thr	Glu	Glu	Thr	Thr	Thr	Gly	Val	His	Arg	Leu	Tyr	His	Phe	Ala		
		200					205					210					
gaa	gaa	ggc	gtg	ctg	cct	tta	cca	ggg	atg	aac	gtc	aac	gac	gct	gtc	787	
Glu	Glu	Gly	Val	Leu	Pro	Phe	Pro	Ala	Met	Asn	Val	Asn	Asp	Ala	Val		
	215					220					225						
acc	aag	tcc	aag	ttt	gat	aac	aag	tac	ggc	acc	cgc	cac	tcc	ctg	atc	835	
Thr	Lys	Ser	Lys	Phe	Asp	Asn	Lys	Tyr	Gly	Thr	Arg	His	Ser	Leu	Ile		
	230					235				240				245			
gac	ggc	atc	aac	cgc	gcc	act	gac	atg	ctc	atg	ggc	ggc	aag	aac	gtg	883	
Asp	Gly	Ile	Asn	Arg	Ala	Thr	Asp	Met	Leu	Met	Gly	Gly	Lys	Asn	Val		
			250					255					260				
ctt	gtc	tgc	ggg	tac	ggc	gat	gtc	ggc	aag	ggc	tgc	gct	gag	gct	tta	931	
Leu	Val	Cys	Gly	Tyr	Gly	Asp	Val	Gly	Lys	Gly	Cys	Ala	Glu	Ala	Phe		

265	270	275	
gac ggc cag ggc gct cgc gtc aag gtc acc gaa gct gac cca atc aac			979
Asp Gly Gln Gly Ala Arg Val Lys Val Thr Glu Ala Asp Pro Ile Asn			
280	285	290	
gct ctt cag gct ctg atg gat ggc tac tct gtg gtc acc gtt gat gag			1027
Ala Leu Gln Ala Leu Met Asp Gly Tyr Ser Val Val Thr Val Asp Glu			
295	300	305	
gac atc gag gac gcc gac atc gtg atc acc ggc acc ggc aac aag gac			1075
Ala Ile Glu Asp Ala Asp Ile Val Ile Thr Ala Thr Gly Asn Lys Asp			
310	315	320	325
atc att tcc ttc gag cag atg ctc aag atg aag gat cac gct ctg ctg			1123
Ile Ile Ser Phe Glu Gln Met Leu Lys Met Lys Asp His Ala Leu Leu			
330	335	340	
ggc aac atc ggt cag ttt gat aat gag atc gat atg cat tcc ctg ttg			1171
Gly Asn Ile Gly His Phe Asp Asn Glu Ile Asp Met His Ser Leu Leu			
345	350	355	
cac ggc gag gac gtc acc cgc acc aag atc aag cca cag atc gag gag			1219
His Arg Asp Asp Val Thr Arg Thr Thr Ile Lys Pro Gln Val Asp Glu			
360	365	370	
ctc acc ttc ttc acc ggt cgc tcc atc atc gtc ctg tcc cca ggt ggt			1267
Phe Thr Phe Ser Thr Gly Arg Ser Ile Ile Val Leu Ser Glu Gly Arg			
375	380	385	
ctg atc aac ctt ggc aac gcc acc gga cag cca tca ttt gtc atg tcc			1315
Leu Leu Asn Leu Gly Asn Ala Thr Gly His Pro Ser Phe Val Met Ser			
390	395	400	405
aac tct ttc gcc gat cag acc att ggc cag atc gaa ctg ttc caa aac			1363
Asn Ser Phe Ala Asp Gln Thr Ile Ala Gln Ile Glu Leu Phe Gln Asn			
410	415	420	
gaa gga cag tac gag aac gag gtc tac cgt ctg			1396
Glu Gly Gln Tyr Glu Asn Glu Val Tyr Arg Leu			
425	430		

0210-102

0211-432

0212-PET

0213-Corynebacterium glutamicum

0400-102

Met Ala Gln Val Met Asp Phe Lys Val Ala Asp Leu Ser Leu Ala Glu
1 5 10 15

Ala Gly Arg His Gln Ile Arg Leu Ala Glu Tyr Glu Met Pro Gly Leu
20 25 30

Met Gln Leu Arg Lys Glu Phe Ala Asp Glu Gln Pro Leu Lys Gly Ala
35 40 45

Arg Ile Ala Gly Ser Ile His Met Thr Val Gln Thr Ala Val Leu Ile
50 55 60

Glu Thr Leu Thr Ala Leu Gly Ala Glu Val Arg Trp Ala Ser Cys Asn
 65 70 75 30
 Ile Phe Ser Thr Gln Asp Glu Ala Ala Ala Ala Ile Val Val Gly Ser
 85 90 95
 Gly Thr Val Glu Glu Pro Ala Gly Val Pro Val Phe Ala Trp Lys Gly
 100 105 110
 Glu Ser Leu Glu Glu Tyr Trp Trp Cys Ile Asn Gln Ile Phe Ser Trp
 115 120 125
 Gly Asp Glu Leu Pro Asn Met Ile Leu Asp Asp Gly Gly Asp Ala Thr
 130 135 140
 Met Ala Val Ile Arg Gly Arg Glu Tyr Glu Gln Ala Gly Leu Val Pro
 145 150 155 160
 Pro Ala Glu Ala Asn Asp Ser Asp Glu Tyr Ile Ala Phe Leu Gly Met
 165 170 175
 Leu Arg Glu Val Leu Ala Ala Glu Pro Gly Lys Trp Gly Lys Ile Ala
 180 185 190
 Glu Ala Val Lys Gly Val Thr Glu Glu Thr Thr Thr Gly Val His Arg
 195 200 205
 Leu Tyr His Phe Ala Glu Glu Gly Val Leu Pro Phe Pro Ala Met Asn
 210 215 220
 Val Asn Asp Ala Val Thr Lys Ser Lys Phe Asp Asn Lys Tyr Gly Thr
 225 230 235 240
 Arg His Ser Leu Ile Asp Gly Ile Asn Arg Ala Thr Asp Met Leu Met
 245 250 255
 Gly Gly Lys Asn Val Leu Val Cys Gly Tyr Gly Asp Val Gly Lys Gly
 260 265 270
 Cys Ala Glu Ala Phe Asp Gly Gln Gly Ala Arg Val Lys Val Thr Glu
 275 280 285
 Ala Asp Pro Ile Asn Ala Leu Gln Ala Leu Met Asp Gly Tyr Ser Val
 290 295 300
 Val Thr Val Asp Glu Ala Ile Glu Asp Ala Asp Ile Val Ile Thr Ala
 305 310 315 320
 Thr Gly Asn Lys Asp Ile Ile Ser Phe Glu Gln Met Leu Lys Met Lys
 325 330 335
 Asp His Ala Leu Leu Gly Asn Ile Gly His Phe Asp Asn Glu Ile Asp
 340 345 350
 Met His Ser Leu Leu His Arg Asp Asp Val Thr Arg Thr Thr Ile Lys
 355 360 365
 Pro Gln Val Asp Glu Phe Thr Phe Ser Thr Gly Arg Ser Ile Ile Val
 370 375 380
 Leu Ser Glu Gly Arg Leu Leu Asn Leu Gly Asn Ala Thr Gly His Pro

385

390

395

400

Ser Phe Val Met Ser Asn Ser Phe Ala Asp Gln Thr Ile Ala Gln Ile
405 410 415

Glu Leu Phe Gln Asn Glu Gly Gln Tyr Glu Asn Glu Val Tyr Arg Leu
420 425 430

<210> 103

<211> 2358

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> 1(1)..(2355)

<223> RXN02085

<400> 103

gacccggtga ttctcggaac ctctgaacat cgtcagaaga ttgcggtgag tcttagccgg 60

gacccggaag ttccggtcaa gcagaaagtc ttttaactcac atg act tcc aac ttt 115
Met Thr Ser Asn Phe
1 5

tct tcc act gtc ggt ggt att cct cgc atc gga ggt aag cgt gaa ctg 165
Ser Ser Thr Val Ala Gly Leu Pro Arg Ile Gly Ala Lys Arg Glu Leu
10 15 20

aag ttc ggg ctc gaa gga tac tgg aat gga tca att gaa ggt cgc gaa 211
Lys Phe Ala Leu Glu Gly Tyr Trp Asn Gly Ser Ile Glu Gly Arg Glu
25 30 35

ctt gca cag acc gcc cgc caa ttg gtc aac act gca tgg gat tct ttg 259
Leu Ala Gln Thr Ala Arg Gln Leu Val Asn Thr Ala Ser Asp Ser Leu
40 45 50

tct gga ttg gat tcc gtt ccg ttt gca gga cgt tcc tac tac gac gca 307
Ser Gly Leu Asp Ser Val Pro Phe Ala Gly Arg Ser Tyr Tyr Asp Ala
55 60 65

atg ctc gat acc gcc gct att ttg ggt gtg ctg ccg gag cgt ttt gat 355
Met Leu Asp Thr Ala Ala Ile Leu Gly Val Leu Pro Glu Arg Phe Asp
70 75 80 85

gac atc got gat cat gaa aac gat ggt ctc cca ctg tgg att gac cgc 403
Asp Ile Ala Asp His Glu Asn Asp Gly Leu Pro Leu Trp Ile Asp Arg
90 95 100

tac ttt ggc gct gct cgc ggt act gag acc ctg cct gca cag gca atg 451
Tyr Phe Gly Ala Ala Arg Gly Thr Glu Thr Leu Pro Ala Gln Ala Met
105 110 115

acc aag tgg ttt gat acc aac tac cac tac ctc gtg ccg gag ttg tct 499
Thr Lys Trp Phe Asp Thr Asn Tyr His Tyr Leu Val Pro Glu Leu Ser
120 125 130

ggg gat aca cgt ttc gtt ttg gat ggc tcc ggc ctg att gag gat ctc 547
Ala Asp Thr Arg Phe Val Leu Asp Ala Ser Ala Leu Ile Glu Asp Leu
135 140 145

cgT tgc cag cag gtt cgt ggc gtt aat gcc cgc cct gtt ctg gtt ggt Arg Cys Gln Gln Val Arg Gly Val Asn Ala Arg Pro Val Leu Val Gly 150 155 160 165	595
cca ctg act ttc ctt tcc ctt gct cgc acc act gat ggt tcc aat cct Pro Leu Thr Phe Leu Ser Leu Ala Arg Thr Thr Asp Gly Ser Asn Pro 170 175 180	643
ttg gat cac ctg cct gca ctg ttt gag gtc tac gag cgc ctc atc aag Leu Asp His Leu Pro Ala Leu Phe Glu Val Tyr Glu Arg Leu Ile Lys 185 190 195	691
tct ttc gat act gag tgg gtt cag atc gat gag cct gag ttg gtc acc Ser Phe Asp Thr Glu Trp Val Gln Ile Asp Glu Pro Ala Leu Val Thr 200 205 210	739
gat gtt gct cct gag gtt ttg gag cca gtc cgc gct ggt tac acc act Asp Val Ala Pro Glu Val Leu Glu Gln Val Arg Ala Gly Tyr Thr Thr 215 220 225	787
ttg gct aag cgc gat gac gtg ttt gtc aat act tac ttc ggc tct gcc Leu Ala Lys Arg Asp Gly Val Phe Val Asn Thr Tyr Phe Gly Ser Gly 230 235 240 245	835
gat cag gct ctg aac act ctt ggt ggc atc ggc ttt ggt gag att gag Asp Gln Ala Leu Asn Thr Leu Ala Gly Ile Gly Leu Gly Ala Ile Gly 250 255 260	883
gta gac ttg gtc acc cat ggc gtc act gag ctt gct gag tgg aag ggt Val Asp Leu Val Thr His Gly Val Thr Glu Leu Ala Ala Trp Lys Gly 265 270 275	931
gag gag ctg ctg gtt ggc ggc atc gtt gat ggt cgt aac att tgg cgc Glu Glu Leu Leu Val Ala Gly Ile Val Asp Gly Arg Asn Ile Trp Arg 280 285 290	979
acc gac ctg tgt gct gct ctt gct tcc ctg aag cgc ctg gca gct cgc Thr Asp Leu Cys Ala Ala Leu Ala Ser Leu Lys Arg Leu Ala Ala Arg 295 300 305	1027
ggc cca atc gca gtg tct acc tct tgt tca ctg ctg cac gtt cct tac Gly Pro Ile Ala Val Ser Thr Ser Cys Ser Leu Leu His Val Pro Tyr 310 315 320 325	1075
acc ctc gag gct gag aac att gag cct gag gtc cgc gac tgg ctt gcc Thr Leu Glu Ala Glu Asn Ile Glu Pro Glu Val Arg Asp Trp Leu Ala 330 335 340	1123
ctc ggc tgg gag aag atc acc gag gtc aag ctg ctt gcc gac gcc cta Phe Gly Ser Glu Lys Ile Thr Glu Val Lys Leu Leu Ala Asp Ala Leu 345 350 355	1171
gcc ggc aac atc gac gcg gct gcg ttc gat gcg gcg tcc gca gca att Ala Gly Asn Ile Asp Ala Ala Phe Asp Ala Ala Ser Ala Ala Ile 360 365 370	1219
gct tct cga cgc acc tcc cca cgc acc gca cca atc aag cag gaa ctc Ala Ser Arg Arg Thr Ser Pro Arg Thr Ala Pro Ile Thr Gln Glu Leu 375 380 385	1267

cct ggc cgt agc cgt gga tcc ttc gac act cgt gtt acg ctg cag gag	1315
Pro Gly Arg Ser Arg Gly Ser Phe Asp Thr Arg Val Thr Leu Gln Glu	
390 395 400 405	
aag tca ctg gag ctt cca gct ctg cca acc acc att ggt tct ttc	1363
Lys Ser Leu Glu Leu Pro Ala Leu Pro Thr Thr Ile Gly Ser Phe	
410 415 420	
cca cag acc cca tcc att cgt tct gct cgc gct cgt ctg cgc aag gaa	1411
Pro Gln Thr Pro Ser Ile Arg Ser Ala Arg Ala Arg Leu Arg Lys Glu	
425 430 435	
tcc acc act tgg gag cag tac gaa gag gca atg cgc gaa gaa atc gat	1459
Ser Ile Thr Leu Glu Gln Tyr Glu Gln Ala Met Arg Glu Gln Ile Asp	
440 445 450	
ctg gcc acc gcc aag cag gaa gaa ctt ggt ctt gat gtg ttg gtt ctc	1507
Leu Val Ile Ala Lys Gln Gln Glu Leu Gly Leu Asp Val Leu Val His	
455 460 465	
ggt gag cca gag cgc aac gac atg gtc cag tac ttc tct gaa ctt ctc	1555
Gly Gln Pro Glu Arg Asn Asp Met Val Gln Tyr Phe Ser Gln Leu Leu	
470 475 480 485	
gac ggt ttc ttc tca acc gcc aac gcc tgg gac gac caa agc tac ggc ttc	1603
Asp Gly Phe Leu Ser Thr Ala Asn Gly Trp Val Gln Ser Tyr Gly Ser	
490 495 500	
cgc cgt gcc cgt cct cca gcc tgg ttc gga aac gtt tcc cgc cca gcc	1651
Arg Lys Val Arg Pro Pro Val Leu Phe Gly Asn Val Ser Arg Pro Ala	
505 510 515	
cca atg act gtc aag tgg ttc cag tac gca cag agc ctg acc cag aag	1699
Pro Met Thr Val Lys Trp Phe Gln Tyr Ala Gln Ser Leu Thr Gln Lys	
520 525 530	
cac tcc aag gga atg ctg acc ggt cca gtc aac atc ctt gaa tgg ttc	1747
His Val Lys Gly Met Leu Thr Gly Pro Val Thr Ile Leu Ala Trp Ser	
535 540 545	
tcc cct cgc gat gat cag cag tgg gct acc aac gct gac cag gtt gaa	1795
Phe Val Arg Asp Asp Gln Pro Leu Ala Thr Thr Ala Asp Gln Val Ala	
550 555 560 565	
ctg gca ctg cgc gat gaa att aac gat ctc atc gag gct ggc gcc aag	1843
Leu Ala Leu Arg Asp Glu Ile Asn Asp Leu Ile Glu Ala Gly Ala Lys	
570 575 580	
atc acc cag ttg gat gag cct cgc att cgt gaa ctg ttg ccc cta cga	1891
Ile Ile Gln Val Asp Glu Pro Ala Ile Arg Glu Leu Leu Pro Leu Arg	
585 590 595	
gac ctc gat aag cct gcc tac ctg cag tgg tcc ttg gac tcc ttc cgc	1939
Asp Val Asp Lys Pro Ala Tyr Leu Gln Trp Ser Val Asp Ser Phe Arg	
600 605 610	
ctg gcc act gcc ggc gca ccc gac gac gtc caa atc caa acc caa atg	1987
Leu Ala Thr Ala Gly Ala Pro Asp Asp Val Gln Ile His Thr His Met	
615 620 625	
tgc tac tcc gag ttc aac gaa gtg atc tcc tgg gtc atc gcc ttg gat	2035

Cys Tyr Ser Glu Phe Asn Glu Val Ile Ser Ser Val Ile Ala Leu Asp
 630 635 640 645
 ggc gat gtc acc acc atc gaa gca gca cgt tcc gac atg cag gtc ctc 2083
 Ala Asp Val Thr Thr Ile Glu Ala Ala Arg Ser Asp Met Gln Val Leu
 650 655 660
 gct ggt ctg aaa tct tcc gcc ttc gag ctc gcc gtc gga cct ggt gtg 2131
 Ala Ala Leu Lys Ser Ser Gly Phe Glu Leu Gly Val Gly Pro Gly Val
 665 670 675
 tgg gat atc cac tcc ccg cgc gtt cct tcc gcg cag aaa gtg gac ggt 2179
 Trp Asp Ile His Ser Pro Arg Val Pro Ser Ala Gln Lys Val Asp Gly
 680 685 690
 ctc ctc gag ggt gca ctg cag tcc gtg gat cct cgc cag ctg tgg gtc 2227
 Leu Leu Glu Ala Ala Leu Gln Ser Val Asp Pro Arg Gln Leu Trp Val
 695 700 705
 aac cca gac tgt ggt ctg aag acc cgt gga tgg cca gaa gtg gaa gtt 2275
 Asn Pro Asp Cys Gly Leu Lys Thr Arg Gly Trp Pro Glu Val Glu Ala
 710 715 720 725
 tcc cta aag gtt ctc gtt gag tcc gct aag cag gct cgt gag aaa atc 2323
 Ser Leu Lys Val Leu Val Gln Ser Ala Lys Gln Ala Arg Glu Lys Ile
 730 735 740
 gga gca act ttc taaattgggt taccgtagg aac 2355
 Gly Ala Thr Ile 745
 <210> 104
 <211> 745
 <212> FRT
 <213> Corynebacterium glutamicum
 <400> 104
 Met Thr Ser Asn Phe Ser Ser Thr Val Ala Gly Leu Pro Arg Ile Gly
 1 5 10 15
 Ala Lys Arg Glu Leu Lys Phe Ala Leu Glu Gly Tyr Trp Asn Gly Ser
 20 25 30
 Ile Glu Gly Arg Glu Leu Ala Gln Thr Ala Arg Gln Leu Val Asn Thr
 35 40 45
 Ala Ser Asp Ser Leu Ser Gly Leu Asp Ser Val Pro Phe Ala Gly Arg
 50 55 60
 Ser Tyr Tyr Asp Ala Met Leu Asp Thr Ala Ala Ile Leu Gly Val Leu
 65 70 75 80
 Pro Glu Arg Phe Asp Asp Ile Ala Asp His Glu Asn Asp Gly Leu Pro
 85 90 95
 Leu Trp Ile Asp Arg Tyr Phe Gly Ala Ala Arg Gly Thr Glu Thr Leu
 100 105 110
 Pro Ala Gln Ala Met Thr Lys Trp Phe Asp Thr Asn Tyr His Tyr Leu
 115 120 125

Val Pro Glu Leu Ser Ala Asp Thr Arg Phe Val Leu Asp Ala Ser Ala
 130 135 140
 Leu Ile Glu Asp Leu Arg Cys Gln Gln Val Arg Gly Val Asn Ala Arg
 145 150 155 160
 Pro Val Leu Val Gly Pro Leu Thr Phe Leu Ser Leu Ala Arg Thr Thr
 165 170 175
 Asp Gly Ser Asn Pro Leu Asp His Leu Pro Ala Leu Phe Glu Val Tyr
 180 185 190
 Glu Arg Leu Ile Lys Ser Phe Asp Thr Glu Trp Val Gln Ile Asp Glu
 195 200 205
 Pro Ala Leu Val Thr Asp Val Ala Pro Glu Val Leu Glu Gln Val Arg
 210 215 220
 Ala Gly Tyr Thr Thr Leu Ala Lys Arg Asp Gly Val Phe Val Asn Thr
 225 230 235 240
 Tyr Phe Gly Ser Gly Asp Gln Ala Leu Asn Thr Leu Ala Gly Ile Gly
 245 250 255
 Leu Gly Ala Ile Gly Val Asp Leu Val Thr His Gly Val Thr Glu Leu
 260 265 270
 Ala Ala Trp Lys Gly Glu Glu Leu Leu Val Ala Gly Ile Val Asp Gly
 275 280 285
 Arg Asn Ile Trp Arg Thr Asp Leu Cys Ala Ala Leu Ala Ser Leu Lys
 290 295 300
 Arg Leu Ala Ala Arg Gly Pro Ile Ala Val Ser Thr Ser Cys Ser Leu
 305 310 315 320
 Leu His Val Pro Tyr Thr Leu Glu Ala Glu Asn Ile Glu Pro Glu Val
 325 330 335
 Arg Asp Trp Leu Ala Phe Gly Ser Glu Lys Ile Thr Glu Val Lys Leu
 340 345 350
 Leu Ala Asp Ala Leu Ala Gly Asn Ile Asp Ala Ala Ala Phe Asp Ala
 355 360 365
 Ala Ser Ala Ala Ile Ala Ser Arg Arg Thr Ser Pro Arg Thr Ala Pro
 370 375 380
 Ile Thr Gln Glu Leu Pro Gly Arg Ser Arg Gly Ser Phe Asp Thr Arg
 385 390 395 400
 Val Thr Leu Gln Glu Lys Ser Leu Glu Leu Pro Ala Leu Pro Thr Thr
 405 410 415
 Thr Ile Gly Ser Phe Pro Gln Thr Pro Ser Ile Arg Ser Ala Arg Ala
 420 425 430
 Arg Leu Arg Lys Glu Ser Ile Thr Leu Glu Gln Tyr Glu Glu Ala Met
 435 440 445

Arg Glu Glu Ile Asp Leu Val Ile Ala Lys Gln Glu Glu Leu Gly Leu
 450 455 460
 Asp Val Leu Val His Gly Glu Pro Glu Arg Asn Asp Met Val Gln Tyr
 465 470 475 480
 Phe Ser Glu Leu Leu Asp Gly Phe Leu Ser Thr Ala Asn Gly Trp Val
 485 490 495
 Gln Ser Tyr Gly Ser Arg Cys Val Arg Pro Pro Val Leu Phe Gly Asn
 500 505 510
 Val Ser Arg Pro Ala Pro Met Thr Val Lys Trp Phe Gln Tyr Ala Gln
 515 520 525
 Ser Leu Thr Gln Lys His Val Lys Gly Met Leu Thr Gly Pro Val Thr
 530 535 540
 Ile Leu Ala Trp Ser Phe Val Arg Asp Asp Gln Pro Leu Ala Thr Thr
 545 550 555 560
 Ala Asp Gln Val Ala Leu Ala Leu Arg Asp Glu Ile Asn Asp Leu Ile
 565 570 575
 Glu Ala Gly Ala Lys Ile Ile Gln Val Asp Glu Pro Ala Ile Arg Glu
 580 585 590
 Leu Leu Pro Leu Arg Asp Val Asp Lys Pro Ala Tyr Leu Gln Trp Ser
 595 600 605
 Val Asp Ser Phe Arg Leu Ala Thr Ala Gly Ala Pro Asp Asp Val Gln
 610 615 620
 Ile His Thr His Met Cys Tyr Ser Glu Phe Asn Glu Val Ile Ser Ser
 625 630 635 640
 Val Ile Ala Leu Asp Ala Asp Val Thr Thr Ile Glu Ala Ala Arg Ser
 645 650 655
 Asp Met Gln Val Leu Ala Ala Leu Lys Ser Ser Gly Phe Glu Leu Gly
 660 665 670
 Val Gly Pro Gly Val Trp Asp Ile His Ser Pro Arg Val Pro Ser Ala
 675 680 685
 Gln Lys Val Asp Gly Leu Leu Glu Ala Ala Leu Gln Ser Val Asp Pro
 690 695 700
 Arg Gln Leu Trp Val Asn Pro Asp Cys Gly Leu Lys Thr Arg Gly Trp
 705 710 715 720
 Pro Glu Val Glu Ala Ser Leu Lys Val Leu Val Glu Ser Ala Lys Gln
 725 730 735
 Ala Arg Glu Lys Ile Gly Ala Thr Ile
 740 745

<210> 105
 <211> 1923
 <212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1900)

<223> FRXA02085

<400> 105

```

caccgggtga ttccgcgaac cttgaaacat cgtcagaaga ttgcggtgag tcttagcggg 60
gatccgcacg ttccggtcaa gcagaaagtc tttaactaac atg act tcc aac ttt 115
Met Thr Ser Asn Phe
1 5

tct tcc act gtc gct ggt ctt cct cgc atc gga gcg aag cgt gaa ctg 163
Ser Ser Thr Val Ala Gly Leu Pro Arg Ile Gly Ala Lys Arg Glu Leu
10 15 20

aag ttc gag ctg gaa ggc tac tgg aat gga tca att gaa ggt ttc gaa 211
Lys Phe Ala Leu Glu Gly Tyr Trp Asn Gly Ser Ile Glu Gly Arg Glu
25 30 35

ctt gcg cag acc gac cgc caa ttg gtc aac att gba tgg gat ttc ttg 259
Leu Ala Gln Thr Ala Arg Gln Leu Val Asn Thr Ala Ser Asp Ser Leu
40 45 50

tct gga ttg gat tcc gtt ccg ttt gca gga cgt tcc tac tac gac gca 307
Ser Gly Leu Asp Ser Val Pro Phe Ala Gly Arg Ser Tyr Tyr Asp Ala
55 60 65

atg ctg gat acc gac gct att ttg ggt atg ctg ccg gag cgt ttc gat 355
Met Leu Asp Thr Ala Ala Ile Leu Gly Val Leu Pro Glu Arg Phe Asp
70 75 80 85

gac atc gct gat cat gaa aac gat ggt ctg cca ctg tgg att gac cgc 403
Asp Ile Ala Asp His Glu Asn Asp Gly Leu Pro Leu Trp Ile Asp Arg
90 95 100

tac ttt ggc gct gct cgc ggt act gag acc ctg cct gca cag gca atg 451
Tyr Phe Gly Ala Ala Arg Gly Thr Glu Thr Leu Pro Ala Gln Ala Met
105 110 115

acc aag tgg ttt gat acc aac tac cac tac ctg gtg ccg gag ttg tct 499
Thr Lys Trp Phe Asp Thr Asn Tyr His Tyr Leu Val Pro Glu Leu Ser
120 125 130

gcg gat aca cgt ttc gtt ttg gat gcg tcc gcg ctg att gag gat ctg 547
Ala Asp Thr Arg Phe Val Leu Asp Ala Ser Ala Leu Ile Glu Asp Leu
135 140 145

cgt tgc cag cag gtt cgt ggc gtt aat gcc cgc cct gtt ctg gtt ggt 595
Arg Cys Gln Gln Val Arg Gly Val Asn Ala Arg Pro Val Leu Val Gly
150 155 160 165

cca ctg act ttc ctt tcc ctt gct cgc acc act gat ggt tcc aat cct 643
Pro Leu Thr Phe Leu Ser Leu Ala Arg Thr Thr Asp Gly Ser Asn Pro
170 175 180

ttg gat cac ctg cct gca ctg ttt gag gtc tac gag cgc ctg atc aag 691
Leu Asp His Leu Pro Ala Leu Phe Glu Val Tyr Glu Arg Leu Ile Lys
185 190 195

```

tct ttc gat act gag tgg gtt cag atc gat gag cct gag ttg gtc acc	739
Ser Phe Asp Thr Glu Trp Val Gln Ile Asp Glu Pro Ala Leu Val Thr	
200 205 210	
gat gtt get cct gag gtt ttg gag cag gtc cgc get ggt tac acc act	787
Asp Val Ala Pro Glu Val Leu Glu Gln Val Arg Ala Gly Tyr Thr Thr	
215 220 225	
ttg gct aag cgc gat ggc gtg ttt gtc aat act tac ttc ggc tct ggc	835
Leu Ala Lys Arg Asp Gly Val Phe Val Asn Thr Tyr Phe Gly Ser Gly	
230 235 240 245	
gat cag gag ctg aac act ctt gag ggc atc ggc ctt ggc gag att ggc	883
Asp Gln Ala Leu Asn Thr Leu Ala Gly Ile Gly Leu Gly Ala Ile Gly	
250 255 260	
ggt gac ttg gtc acc cat ggc gtc act gag ctt get gag tgg aag ggt	931
Val Asp Leu Val Thr His Gly Val Thr Glu Leu Ala Ala Trp Lys Gly	
265 270 275	
cag gag ctg ctg gtt cgc ggc atc gtt gat ggt cgt aac att tgg cgc	979
Glu Glu Leu Leu Val Ala Gly Ile Val Asp Gly Arg Asn Ile Trp Arg	
280 285 290	
acc aac att tgt get act ctt get tcc ctg aag cgc ctt gca gat cgc	1027
Thr Asp Leu Cys Ala Ala Leu Ala Ser Leu Lys Arg Leu Ala Ala Arg	
295 300 305	
ggc cca att gca gtg tct acc tct tgt tca ctg ctg cca gtt cct tac	1075
Gly Pro Ile Ala Val Ser Thr Ser Cys Ser Leu Leu His Val Pro Tyr	
310 315 320 325	
acc ttc gag get gag aac att gag cct gag gtc cgc gac tgg att ggc	1123
Thr Leu Glu Ala Glu Asn Ile Glu Pro Glu Val Arg Asp Trp Leu Ala	
330 335 340	
ttc ggc tcc gag aag atc acc gag gtc aag ctg ctt gcc gac gcc cta	1171
Phe Gly Ser Glu Lys Ile Thr Glu Val Lys Leu Leu Ala Asp Ala Leu	
345 350 355	
gcc cgc aac atc gac ggc get ggc ttc gat ggc ggc tcc gca gca att	1219
Ala Gly Asn Ile Asp Ala Ala Ala Phe Asp Ala Ala Ser Ala Ala Ile	
360 365 370	
get tct cga cgc acc tcc cca cgc acc gca cca atc acg cag gaa ctc	1267
Ala Ser Arg Arg Thr Ser Pro Arg Thr Ala Pro Ile Thr Gln Glu Leu	
375 380 385	
cct ggc cgt agc cgt gga tcc ttc gac act cgt gtt acg ctg cag gag	1315
Pro Gly Arg Ser Arg Gly Ser Phe Asp Thr Arg Val Thr Leu Gln Glu	
390 395 400 405	
aag tca ctg gag ctt cca get ctg cca acc acc acc att ggt tct ttc	1363
Lys Ser Leu Glu Leu Pro Ala Leu Pro Thr Thr Thr Ile Gly Ser Phe	
410 415 420	
cca cag acc cca tcc att cgt tct get cgc get cgt ctg cgc aag gaa	1411
Pro Gln Thr Pro Ser Ile Arg Ser Ala Arg Ala Arg Leu Arg Lys Glu	
425 430 435	

tcc atc act ttg gag cag tac gaa gag gca atg cgc gaa gaa atc gat 1459
 Ser Ile Thr Leu Glu Gln Tyr Glu Glu Ala Met Arg Glu Glu Ile Asp
 440 445 450

ctg gtc atc gcc aag cag gaa gaa ctt ggt ctt gat gtg ttg gtt cac 1507
 Leu Val Ile Ala Lys Gln Glu Glu Leu Gly Leu Asp Val Leu Val His
 455 460 465

ggt gag cca gag cgc aac gac atg gtt cag tac ttc tct gaa ctt ctc 1555
 Gly Glu Pro Glu Arg Asn Asp Met Val Gln Tyr Phe Ser Glu Leu Leu
 470 475 480 485

gac ggt ttc ctc tca aac gcc aac ggc tgg gtc cca agc tac ggc tcc 1603
 Asp Gly Phe Leu Ser Thr Ala Asn Gly Trp Val Gln Ser Tyr Gly Ser
 490 495 500

cgc tgt gtt cgt cct cca gtg ttg ttc gga aac gtt tcc cgt cca ggc 1651
 Arg Cys Val Arg Pro Pro Val Leu Phe Gly Asn Val Ser Arg Pro Ala
 505 510 515

cca atg act gtc aag tgg ttc cag tac gca cag agc ctg acc cag aag 1699
 Pro Met Thr Val Lys Trp Phe Gln Tyr Ala Gln Ser Leu Thr Gln Lys
 520 525 530

cat gtc aac gga atg ctc acc ggt cca gtc acc atc att gca tgg tcc 1747
 His Val Lys Gly Met Leu Thr Gly Pro Val Thr Ile Leu Ala Trp Ser
 535 540 545

ttc gtt cgt gat gat cag cag atg ggt acc act ggt gac cag gtt gca 1795
 Phe Val Arg Asp Asp Gln Pro Leu Ala Thr Thr Ala Asp Gln Val Ala
 550 555 560 565

ctg gca ctg cgc gat gaa att aac gat ctc atc gag gct ggt ggc aag 1843
 Leu Ala Leu Arg Asp Glu Ile Asn Asp Leu Ile Glu Ala Gly Ala Lys
 570 575 580

atc atc cag gtg gat gag cct ggc att cgt gaa ctg ttg ccc gct aag 1891
 Ile Ile Gln Val Asp Glu Pro Ala Ile Arg Glu Leu Leu Pro Ala Thr
 585 590 595

aga cgt cga taagcctgcc tacctgcagt ggt 1923
 Arg Arg Arg
 600

<210> 106

<211> 600

<212> PRT

<213> Corynebacterium glutamicum

<400> 106

Met Thr Ser Asn Phe Ser Ser Thr Val Ala Gly Leu Pro Arg Ile Gly
 1 5 10 15

Ala Lys Arg Glu Leu Lys Phe Ala Leu Glu Gly Tyr Trp Asn Gly Ser
 20 25 30

Ile Glu Gly Arg Glu Leu Ala Gln Thr Ala Arg Gln Leu Val Asn Thr
 35 40 45

Ala Ser Asp Ser Leu Ser Gly Leu Asp Ser Val Pro Phe Ala Gly Arg

50	55	60
Ser Tyr Tyr Asp Ala Met Leu Asp Thr Ala Ala Ile Leu Gly Val Leu 65 70 75 80		
Pro Glu Arg Phe Asp Asp Ile Ala Asp His Glu Asn Asp Gly Leu Pro 85 90 95		
Leu Trp Ile Asp Arg Tyr Phe Gly Ala Ala Arg Gly Thr Glu Thr Leu 100 105 110		
Pro Ala Gln Ala Met Thr Lys Trp Phe Asp Thr Asn Tyr His Tyr Leu 115 120 125		
Val Pro Glu Leu Ser Ala Asp Thr Arg Phe Val Leu Asp Ala Ser Ala 130 135 140		
Leu Ile Glu Asp Leu Arg Cys Gln Gln Val Arg Gly Val Asn Ala Arg 145 150 155 160		
Pro Val Leu Val Gly Pro Leu Thr Phe Leu Ser Leu Ala Arg Thr Thr 165 170 175		
Asp Gly Ser Asn Pro Leu Asp His Leu Pro Ala Leu Phe Gln Val Tyr 180 185 190		
Glu Arg Leu Ile Lys Ser Phe Asp Thr Glu Trp Val Gln Ile Asp Glu 195 200 205		
Pro Ala Leu Val Thr Asp Val Ala Pro Glu Val Leu Glu Gln Val Arg 210 215 220		
Ala Gly Tyr Thr Thr Leu Ala Lys Arg Asp Gly Val Phe Val Asn Thr 225 230 235 240		
Tyr Phe Gly Ser Gly Asp Gln Ala Leu Asn Thr Leu Ala Gly Ile Gly 245 250 255		
Leu Gly Ala Ile Gly Val Asp Leu Val Thr His Gly Val Thr Glu Leu 260 265 270		
Ala Ala Trp Lys Gly Glu Glu Leu Leu Val Ala Gly Ile Val Asp Gly 275 280 285		
Arg Asn Ile Trp Arg Thr Asp Leu Cys Ala Ala Leu Ala Ser Leu Lys 290 295 300		
Arg Leu Ala Ala Arg Gly Pro Ile Ala Val Ser Thr Ser Cys Ser Leu 305 310 315 320		
Leu His Val Pro Tyr Thr Leu Glu Ala Glu Asn Ile Glu Pro Glu Val 325 330 335		
Arg Asp Trp Leu Ala Phe Gly Ser Glu Lys Ile Thr Glu Val Lys Leu 340 345 350		
Leu Ala Asp Ala Leu Ala Gly Asn Ile Asp Ala Ala Ala Phe Asp Ala 355 360 365		
Ala Ser Ala Ala Ile Ala Ser Arg Arg Thr Ser Pro Arg Thr Ala Pro 370 375 380		

Ile Thr Gln Glu Leu Pro Gly Arg Ser Arg Gly Ser Phe Asp Thr Arg
 385 390 395 400
 Val Thr Leu Gln Glu Lys Ser Leu Glu Leu Pro Ala Leu Pro Thr Thr
 405 410 415
 Thr Ile Gly Ser Phe Pro Gln Thr Pro Ser Ile Arg Ser Ala Arg Ala
 420 425 430
 Arg Leu Arg Lys Glu Ser Ile Thr Leu Glu Gln Tyr Glu Glu Ala Met
 435 440 445
 Arg Glu Glu Ile Asp Leu Val Ile Ala Lys Gln Glu Glu Leu Gly Leu
 450 455 460
 Asp Val Leu Val His Gly Glu Pro Glu Arg Asn Asp Met Val Gln Tyr
 465 470 475 480
 Phe Ser Gln Leu Leu Asp Gly Phe Leu Ser Thr Ala Asn Gly Trp Val
 485 490 495
 Gln Ser Tyr Gly Ser Arg Cys Val Arg Pro Pro Val Leu Phe Gly Asn
 500 505 510
 Val Ser Arg Pro Ala Pro Met Thr Val Lys Trp Phe Gln Tyr Ala Gln
 515 520 525
 Ser Leu Thr Gln Lys His Val Lys Gly Met Leu Thr Gly Pro Val Thr
 530 535 540
 Ile Leu Ala Trp Ser Phe Val Arg Asp Asp Gln Pro Leu Ala Thr Thr
 545 550 555 560
 Ala Asp Gln Val Ala Leu Ala Leu Arg Asp Glu Ile Asn Asp Leu Ile
 565 570 575
 Glu Ala Gly Ala Lys Ile Ile Gln Val Asp Glu Pro Ala Ile Arg Glu
 580 585 590
 Leu Leu Pro Ala Thr Arg Arg Arg
 595 600

<210> 107
 <211> 603
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(580)
 <223> FRXA02086

<400> 107
 gatgatcaga cgttggtac caatgctgac caggttgac tggactgag cgaatgaatt 60
 aacgatctca tcgaggtgg cgcgaagatc atcaggtgg atg agc ctg cga ttc 115
 Met Ser Leu Arg Phe
 1 5

gtg aac tgt tgc ccc cta cga gac gtc gat aag cct gcc tac ctg cag 163
Val Asn Cys Cys Pro Leu Arg Asp Val Asp Lys Pro Ala Tyr Leu Gln
10 15 20

tgg tcc gtg gac tcc ttc cgc ctg ggc act gcc ggc gca ccc gac gac 211
Trp Ser Val Asp Ser Phe Arg Leu Ala Thr Ala Gly Ala Pro Asp Asp
25 30 35

gtc caa atc cac acc cac atg tgc tac tcc gag ttc aac gaa gtg atc 259
Val Gln Ile His Thr His Met Cys Tyr Ser Glu Phe Asn Glu Val Ile
40 45 50

tcc tcc gtc atc gag ttg gat gcc gat gtc acc acc atc gaa gca gaa 307
Ser Ser Val Ile Ala Leu Asp Ala Asp Val Thr Thr Ile Glu Ala Ala
55 60 65

agt tcc gac atg cag gtc ctc gcc gat gtc gaa tct tcc gcc ttc gag 355
Arg Ser Asp Met Gln Val Leu Ala Ala Leu Lys Ser Ser Gly Phe Glu
70 75 80 85

ctc gcc gtc gga cct ggt gtg tgg gat atc ctc tcc ccc cgc gtt cct 403
Leu Gly Val Gly Pro Gly Val Trp Asp Ile His Ser Pro Arg Val Pro
90 95 100

tcc gcc cag aaa gtg gac ggt ctc ctc gag gat gca ctg cag tcc gtg 451
Ser Ala Gln Lys Val Asp Gly Leu Leu Glu Ala Ala Leu Gln Ser Val
105 110 115

gat cct gcc cag ctg tgg gtc aac cca gac tct ggt ctg aag atc cct 499
Asp Pro Arg Gln Leu Trp Val Asn Pro Asp Cys Gly Leu Lys Thr Arg
120 125 130

gga tgg cca gaa gtg gaa gct tcc cta aag gat ctc gtt gag tcc gct 547
Gly Trp Pro Glu Val Glu Ala Ser Leu Lys Val Leu Val Glu Ser Ala
135 140 145

aag cag gct cgt gag aaa atc gga gca act atc taaattgggt taacgctagg 600
Lys Gln Ala Arg Glu Lys Ile Gly Ala Thr Ile
150 155 160

aac 603

<210> 108

<211> 160

<212> PRT

<213> Corynebacterium glutamicum

<400> 108

Met Ser Leu Arg Phe Val Asn Cys Cys Pro Leu Arg Asp Val Asp Lys
1 5 10 15

Pro Ala Tyr Leu Gln Trp Ser Val Asp Ser Phe Arg Leu Ala Thr Ala
20 25 30

Gly Ala Pro Asp Asp Val Gln Ile His Thr His Met Cys Tyr Ser Glu
35 40 45

Phe Asn Glu Val Ile Ser Ser Val Ile Ala Leu Asp Ala Asp Val Thr
50 55 60

Thr Ile Glu Ala Ala Arg Ser Asp Met Gln Val Leu Ala Ala Leu Lys
65 70 75 80

Ser Ser Gly Phe Glu Leu Gly Val Gly Pro Gly Val Trp Asp Ile His
85 90 95

Ser Pro Arg Val Pro Ser Ala Gln Lys Val Asp Gly Leu Leu Glu Ala
100 105 110

Ala Leu Gln Ser Val Asp Pro Arg Gln Leu Trp Val Asn Pro Asp Cys
115 120 125

Gly Leu Lys Thr Arg Gly Trp Pro Glu Val Glu Ala Ser Leu Lys Val
130 135 140

Leu Val Glu Ser Ala Lys Gln Ala Arg Glu Lys Ile Gly Ala Thr Ile
145 150 155 160

<210> 104

<211> 1326

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1303)

<223> EX02643

<400> 109

atgaataaaa ttccgggtgc agtgaccgta ggtgaggtaa acgcgggttag agtcgaatga 60

taatttgata cctctctctcg accttttagat tggattttta atg agt cag aac agc 115
Met Ser Gln Asn Arg
1 5

atc agt acc aat cag gtt ggt tcc ttg ccc cgt acc cca gag cta ctt 163
Ile Arg Thr Thr His Val Gly Ser Leu Pro Arg Thr Pro Glu Leu Leu
10 15 20

gat gca aac atc aag cgt tct aac ggt gag att ggg gag gag gaa ttc 211
Asp Ala Asn Ile Lys Arg Ser Asn Gly Glu Ile Gly Glu Glu Glu Phe
25 30 35

ttc cag att ctg cag tct tct gta gat gac gtg atc aag cgc cag gtt 259
Phe Gln Ile Leu Gln Ser Ser Val Asp Asp Val Ile Lys Arg Gln Val
40 45 50

gac ctg ggt atc gac atc ctt aac gag ggc gaa tac ggc cac gtc acc 307
Asp Leu Gly Ile Asp Ile Leu Asn Glu Gly Glu Tyr Gly His Val Thr
55 60 65

tcc ggt gca gtt gac ttc ggt gca tgg tgg aac tac tcc ttc acc cgc 355
Ser Gly Ala Val Asp Phe Gly Ala Trp Trp Asn Tyr Ser Phe Thr Arg
70 75 80 85

ctg ggc gga ctg acc atg acc gat acc gac cgt tgg gca agc cag gaa 403
Leu Gly Gly Leu Thr Met Thr Asp Thr Asp Arg Trp Ala Ser Gln Glu
90 95 100

gca gtg cgt tcc acc cct ggc aac atc gag ctg acc agc ttc tct gat 451

Ala	Val	Arg	Ser	Thr	Pro	Gly	Asn	Ile	Glu	Leu	Thr	Ser	Phe	Ser	Asp		
			105					110					115				
cg	gc	gac	gc	gca	ttg	ttc	agc	gaa	gca	tac	gag	gat	cca	gta	tot	499	
Arg	Arg	Asp	Arg	Ala	Leu	Phe	Ser	Glu	Ala	Tyr	Glu	Asp	Pro	Val	Ser		
		120					125					130					
ggc	atc	ttc	acc	gg	gc	gct	tct	gtg	ggc	aac	cca	gag	ttc	acc	gga	547	
Gly	Ile	Phe	Thr	Gly	Arg	Ala	Ser	Val	Gly	Asn	Pro	Glu	Phe	Thr	Gly		
	135					140					145						
act	att	acc	tac	att	ggc	cag	gaa	gaa	act	cag	acg	gat	gtt	gat	ctg	595	
Pro	Ile	Thr	Tyr	Ile	Gly	Gln	Glu	Glu	Thr	Gln	Thr	Asp	Val	Asp	Leu		
	150				155					160					165		
ctg	aag	aag	ggc	atg	aac	gca	gcg	gga	gct	acc	gac	ggc	ttc	gtt	gca	643	
Leu	Lys	Lys	Gly	Met	Asn	Ala	Ala	Gly	Ala	Thr	Asp	Gly	Phe	Val	Ala		
				170				175						180			
gaa	cta	tcc	cta	gga	tct	gca	act	aga	ttg	acc	aac	aag	ttc	tac	gac	691	
Ala	Leu	Ser	Pro	Gly	Ser	Ala	Ala	Arg	Leu	Thr	Asn	Lys	Phe	Tyr	Asp		
			185					190					195				
act	gat	gaa	gaa	gtc	gtc	gca	gca	tgt	gct	gat	gcg	ctt	tcc	cag	gaa	739	
Thr	Asp	Glu	Glu	Val	Val	Ala	Ala	Cys	Ala	Asp	Ala	Leu	Ser	Gln	Glu		
	200					205						210					
tac	aag	atc	atc	att	gat	gaa	ggt	ctc	acc	gtt	cag	ctc	gat	gaa	ccg	787	
Tyr	Lys	Ile	Ile	Thr	Asp	Ala	Gly	Leu	Thr	Val	Gln	Leu	Asp	Ala	Pro		
	215					220					225						
gac	ttg	gca	gaa	gca	tgg	gat	cag	atc	aac	cca	gag	cca	agt	gtg	aag	835	
Asp	Leu	Ala	Glu	Ala	Trp	Asp	Gln	Ile	Asn	Pro	Glu	Pro	Ser	Val	Lys		
	230				235					240				245			
gat	tac	ttg	gac	tgg	atc	ggt	aca	cgc	atc	gat	gcc	atc	aac	agt	gca	883	
Asp	Tyr	Leu	Asp	Trp	Ile	Gly	Thr	Arg	Ile	Asp	Ala	Ile	Asn	Ser	Ala		
			250					255						260			
gtg	aag	ggc	ctt	cca	aag	gaa	cag	acc	cgc	ctg	cac	atc	tgc	tgg	ggc	931	
Val	Lys	Gly	Leu	Pro	Lys	Glu	Gln	Thr	Arg	Leu	His	Ile	Cys	Trp	Gly		
			265				270						275				
tct	tgg	cac	gga	cca	cac	gtc	act	gac	atc	cca	ttc	ggt	gac	atc	att	979	
Ser	Trp	His	Gly	Pro	His	Val	Thr	Asp	Ile	Pro	Phe	Gly	Asp	Ile	Ile		
		280				285						290					
ggt	gag	atc	ctg	cgc	gca	gag	gtc	ggt	ggc	ttc	tcc	ctc	gaa	ggc	gca	1027	
Gly	Glu	Ile	Leu	Arg	Ala	Glu	Val	Gly	Gly	Phe	Ser	Phe	Glu	Gly	Ala		
	295					300						305					
tct	cct	cgt	cac	gca	cac	gag	tgg	cgt	gta	tgg	gaa	gaa	aac	aag	ctt	1075	
Ser	Pro	Arg	His	Ala	His	Glu	Trp	Arg	Val	Trp	Glu	Glu	Asn	Lys	Leu		
	310				315					320					325		
cct	gaa	ggc	tct	gtt	atc	tac	cct	ggt	gtt	gtg	tct	cac	tcc	atc	aac	1123	
Pro	Glu	Gly	Ser	Val	Ile	Tyr	Pro	Gly	Val	Val	Ser	His	Ser	Ile	Asn		
			330					335						340			
gct	gtg	gag	cac	cca	cgc	ctg	gtt	gct	gat	cgt	atc	gtt	cag	ttc	gcc	1171	
Ala	Val	Glu	His	Pro	Arg	Leu	Val	Ala	Asp	Arg	Ile	Val	Gln	Phe	Ala		

345 350 355
 aag ctt gtt ggc cct gag aac gtc att ggc tcc act gac tgt ggt ctg 1219
 Lys Leu Val Gly Pro Glu Asn Val Ile Ala Ser Thr Asp Cys Gly Leu
 360 365 370
 ggc gga cgt ctg cat tcc cag atc gca tgg gca aag ctg gag tcc cta 1267
 Gly Gly Arg Leu His Ser Gln Ile Ala Trp Ala Lys Leu Glu Ser Leu
 375 380 385
 gta gag ggc gct cgc att gca tca aag gaa ctg ttc taagctagac 1313
 Val Glu Gly Ala Arg Ile Ala Ser Lys Glu Leu Phe
 390 395 400
 aacgagggtt gat 1326

<210> 110

<211> 401

<212> PRT

<213> Corynebacterium glutamicum

<400> 110

Met Ser Gln Asn Arg Ile Arg Thr Thr His Val Gly Ser Leu Pro Arg
 1 5 10 15
 Thr Pro Glu Leu Leu Asp Ala Asn Ile Lys Arg Ser Asn Gly Glu Ile
 20 25 30
 Gly Glu Glu Glu Phe Phe Gln Ile Leu Gln Ser Ser Val Asp Asp Val
 35 40 45
 Ile Lys Arg Gln Val Asp Leu Gly Ile Asp Ile Leu Asn Glu Gly Glu
 50 55 60
 Tyr Gly His Val Thr Ser Gly Ala Val Asp Phe Gly Ala Trp Trp Asn
 65 70 75 80
 Tyr Ser Phe Thr Arg Leu Gly Gly Leu Thr Met Thr Asp Thr Asp Arg
 85 90 95
 Trp Ala Ser Gln Glu Ala Val Arg Ser Thr Pro Gly Asn Ile Glu Leu
 100 105 110
 Thr Ser Phe Ser Asp Arg Arg Asp Arg Ala Leu Phe Ser Glu Ala Tyr
 115 120 125
 Glu Asp Pro Val Ser Gly Ile Phe Thr Gly Arg Ala Ser Val Gly Asn
 130 135 140
 Pro Glu Phe Thr Gly Pro Ile Thr Tyr Ile Gly Gln Glu Glu Thr Gln
 145 150 155 160
 Thr Asp Val Asp Leu Leu Lys Lys Gly Met Asn Ala Ala Gly Ala Thr
 165 170 175
 Asp Gly Phe Val Ala Ala Leu Ser Pro Gly Ser Ala Ala Arg Leu Thr
 180 185 190
 Asn Lys Phe Tyr Asp Thr Asp Glu Glu Val Val Ala Ala Cys Ala Asp
 195 200 205

Ala Leu Ser Gln Glu Tyr Lys Ile Ile Thr Asp Ala Gly Leu Thr Val
 210 215 220

Gln Leu Asp Ala Pro Asp Leu Ala Glu Ala Trp Asp Gln Ile Asn Pro
 225 230 235 240

Glu Pro Ser Val Lys Asp Tyr Leu Asp Trp Ile Gly Thr Arg Ile Asp
 245 250 255

Ala Ile Asn Ser Ala Val Lys Gly Leu Pro Lys Glu Gln Thr Arg Leu
 260 265 270

His Ile Cys Trp Gly Ser Trp His Gly Pro His Val Thr Asp Ile Pro
 275 280 285

Phe Gly Asp Ile Ile Gly Glu Ile Leu Arg Ala Glu Val Gly Gly Phe
 290 295 300

Ser Phe Glu Gly Ala Ser Pro Arg His Ala His Glu Trp Arg Val Trp
 305 310 315 320

Gln Glu Asn Lys Leu Pro Gln Gly Ser Val Ile Tyr Pro Gly Val Val
 325 330 335

Ser His Ser Ile Asn Ala Val Glu His Pro Arg Leu Val Ala Asp Arg
 340 345 350

Ile Val Gln Phe Ala Lys Leu Val Gly Pro Glu Asn Val Ile Ala Ser
 355 360 365

Thr Asp Cys Gly Leu Gly Gly Arg Leu His Ser Gln Ile Ala Trp Ala
 370 375 380

Lys Leu Glu Ser Leu Val Glu Gly Ala Arg Ile Ala Ser Lys Glu Leu
 385 390 395 400

Phe

<210> 111
 <211> 548
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (1)..(525)
 <223> FRXA02648

<400> 111
 gac gca ccg gac ttg gca gaa gca tgg gat cag atc aac cca gag cca 48
 Asp Ala Pro Asp Leu Ala Glu Ala Trp Asp Gln Ile Asn Pro Glu Pro
 1 5 10 15

agg gtg aag gat tac ttg gac tgg atc ggt aca cgc atc gat gcc atc 96
 Ser Val Lys Asp Tyr Leu Asp Trp Ile Gly Thr Arg Ile Asp Ala Ile
 20 25 30

aac agt gca gtg aag ggc ctt cca aag gaa cag aac cgc ctg cac atc 144

Asn Ser Ala Val Lys Gly Leu Pro Lys Glu Gln Thr Arg Leu His Ile
 35 40 45
 tgc tgg ggc tct tgg cac gga cca cac gtc act gac atc cca ttc ggt 192
 Cys Trp Gly Ser Trp His Gly Pro His Val Thr Asp Ile Pro Phe Gly
 50 55 60
 gac atc att gtt gag atc ctg cgc gca gag gtc gat ggc ttc tcc ttc 240
 Asp Ile Ile Gly Glu Ile Leu Arg Ala Glu Val Gly Gly Phe Ser Phe
 65 70 75 80
 gaa ggc gca tct cct cgt cac gca cac gag tgg cgt gta tgg gaa gaa 288
 Glu Gly Ala Ser Pro Arg His Ala His Glu Trp Arg Val Trp Glu Glu
 85 90 95
 aac aag ctt cct gaa ggc tct gtt atc tac cct ggt gtt gtg tct cac 336
 Asn Lys Leu Pro Gln Gly Ser Val Ile Tyr Pro Gly Val Val Ser His
 100 105 110
 tcc atc aac gtt gtt gag cac cca cgt ctg gtt gtt gat gtt atc gtt 384
 Ser Ile Asn Ala Val Glu His Pro Arg Leu Val Ala Asp Arg Ile Val
 115 120 125
 gag ttc gcc aag ctt gtt ggc cct gag aac gtc att gag tcc act gac 432
 Gln Phe Ala Lys Leu Val Gly Pro Glu Asn Val Ile Ala Ser Thr Asp
 130 135 140
 tgt ggt ctg ggc gga cgt ctg cat tcc cag atc gca tgg gca aag ctg 480
 Cys Gly Leu Gly Gly Arg Leu His Ser Gln Ile Ala Trp Ala Lys Leu
 145 150 155 160
 gag tcc cta gta gag ggc gtc agc att gca tca aag gaa ctg tcc 528
 Glu Ser Leu Val Glu Gly Ala Arg Ile Ala Ser Lys Glu Leu Phe
 165 170 175
 taagctagac aacgagggtt gct 576

<210> 112
 <211> 175
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 112
 Asp Ala Pro Asp Leu Ala Glu Ala Trp Asp Gln Ile Asn Pro Glu Pro
 1 5 10 15
 Ser Val Lys Asp Tyr Leu Asp Trp Ile Gly Thr Arg Ile Asp Ala Ile
 20 25 30
 Asn Ser Ala Val Lys Gly Leu Pro Lys Glu Gln Thr Arg Leu His Ile
 35 40 45
 Cys Trp Gly Ser Trp His Gly Pro His Val Thr Asp Ile Pro Phe Gly
 50 55 60
 Asp Ile Ile Gly Glu Ile Leu Arg Ala Glu Val Gly Gly Phe Ser Phe
 65 70 75 80
 Glu Gly Ala Ser Pro Arg His Ala His Glu Trp Arg Val Trp Glu Glu
 85 90 95

Asn Lys Leu Pro Glu Gly Ser Val Ile Tyr Pro Gly Val Val Ser His
100 105 110

Ser Ile Asn Ala Val Glu His Pro Arg Leu Val Ala Asp Arg Ile Val
115 120 125

Gln Phe Ala Lys Leu Val Gly Pro Glu Asn Val Ile Ala Ser Thr Asp
130 135 140

Cys Gly Leu Gly Gly Arg Leu His Ser Gln Ile Ala Trp Ala Lys Leu
145 150 155 160

Glu Ser Leu Val Glu Gly Ala Arg Ile Ala Ser Lys Glu Leu Phe
165 170 175

<210> 113

<211> 784

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)...(784)

<223> FRMAG0655

<400> 113

atgaataaaaa ttcgggttgc agtgacacgta ggtgaggttaa aagggttag agtcgaatga 60

gagtttgata tttcttttcg acttttagat tggattttca atg agc cag aac cgc 115
Met Ser Gln Asn Arg
1 5

atc agg acc act cac gtt ggt tcc ttg acc cgt acc cca gag cta ctt 163
Ile Arg Thr Thr His Val Gly Ser Leu Pro Arg Thr Pro Glu Leu Leu
10 15 20

gat gca aac atc aag cgt tct aac ggt gag att ggg gag gag gaa ttc 211
Asp Ala Asn Ile Lys Arg Ser Asn Gly Glu Ile Gly Glu Glu Glu Phe
25 30 35

ttc cag att ctg cag tct tct gta gat gac gtg atc aag cgc cag gtt 259
Phe Gln Ile Leu Gln Ser Ser Val Asp Asp Val Ile Lys Arg Gln Val
40 45 50

gac ctg ggt atc gac atc ctt aac gag ggc gaa tac ggc cac gtc acc 307
Asp Leu Gly Ile Asp Ile Leu Asn Glu Gly Glu Tyr Gly His Val Thr
55 60 65

tcc ggt gca gtt gac ttc ggt gca tgg tgg aac tac tcc ttc acc cgc 355
Ser Gly Ala Val Asp Phe Gly Ala Trp Trp Asn Tyr Ser Phe Thr Arg
70 75 80 85

ctg ggc gga ctg acc atg acc gat acc gac cgt tgg gca agc cag gaa 403
Leu Gly Gly Leu Thr Met Thr Asp Thr Asp Arg Trp Ala Ser Gln Glu
90 95 100

gca gtg cgt tcc acc cct ggc aac atc gag ctg acc agc ttc tct gat 461
Ala Val Arg Ser Thr Pro Gly Asn Ile Glu Leu Thr Ser Phe Ser Asp
105 110 115

cgt cgc gac cgc gca ttg ttc agc gaa gca tac gag gat cca gta tct 499
 Arg Arg Asp Arg Ala Leu Phe Ser Glu Ala Tyr Glu Asp Pro Val Ser
 120 125 130

ggc atc ttc acc ggt cgc gct tct gtg ggc aac cca gag ttc acc gga 547
 Gly Ile Phe Thr Gly Arg Ala Ser Val Gly Asn Pro Glu Phe Thr Gly
 135 140 145

cct att acc tac att ggc cag gaa gaa act cag acg gat gtt gat ctg 595
 Pro Ile Thr Tyr Ile Gly Gln Glu Glu Thr Gln Thr Asp Val Asp Leu
 150 155 160 165

ctg aag aag ggc atg aac gca gag gga gct aac gac ggc ttc gtt gca 643
 Leu Lys Lys Gly Met Asn Ala Ala Gly Ala Thr Asp Gly Phe Val Ala
 170 175 180

gca cta tcc cca gga tct gca gct cga ttg aac aac aag ttc tac gac 691
 Ala Leu Ser Pro Gly Ser Ala Ala Arg Leu Thr Asn Lys Phe Tyr Asp
 185 190 195

act gat gaa gaa atc gtc gca gca tct gct gat gct ctt tcc tag gaa 739
 Thr Asp Glu Glu Val Val Ala Ala Cys Ala Asp Ala Leu Ser Gln Glu
 200 205 210

tac aag atc atc acc gat gca ggt ctg acc gtt cag ctc gac gca 784
 Tyr Lys Ile Ile Thr Asp Ala Gly Leu Thr Val Gln Leu Asp Ala
 215 220 225

<210> 114

<211> 128

<212> PRT

<213> Corynebacterium glutamicum

<400> 114

Met Ser Gln Asn Arg Ile Arg Thr Thr His Val Gly Ser Leu Pro Arg
 1 5 10 15

Thr Pro Glu Leu Leu Asp Ala Asn Ile Lys Arg Ser Asn Gly Glu Ile
 20 25 30

Gly Glu Glu Glu Phe Phe Gln Ile Leu Gln Ser Ser Val Asp Asp Val
 35 40 45

Ile Lys Arg Gln Val Asp Leu Gly Ile Asp Ile Leu Asn Glu Gly Glu
 50 55 60

Tyr Gly His Val Thr Ser Gly Ala Val Asp Phe Gly Ala Trp Trp Asn
 65 70 75 80

Tyr Ser Phe Thr Arg Leu Gly Gly Leu Thr Met Thr Asp Thr Asp Arg
 85 90 95

Trp Ala Ser Gln Glu Ala Val Arg Ser Thr Pro Gly Asn Ile Glu Leu
 100 105 110

Thr Ser Phe Ser Asp Arg Arg Asp Arg Ala Leu Phe Ser Glu Ala Tyr
 115 120 125

Glu Asp Pro Val Ser Gly Ile Phe Thr Gly Arg Ala Ser Val Gly Asn

130 135 140
 Pro Glu Phe Thr Gly Pro Ile Thr Tyr Ile Gly Gln Glu Glu Thr Gln
 145 150 155 160
 Thr Asp Val Asp Leu Leu Lys Lys Gly Met Asn Ala Ala Gly Ala Thr
 165 170 175
 Asp Gly Phe Val Ala Ala Leu Ser Pro Gly Ser Ala Ala Arg Leu Thr
 180 185 190
 Asn Lys Phe Tyr Asp Thr Asp Glu Glu Val Val Ala Ala Cys Ala Asp
 195 200 205
 Ala Leu Ser Gln Glu Tyr Lys Ile Ile Thr Asp Ala Gly Leu Thr Val
 210 215 220
 Gln Leu Asp Ala
 225

<210> 115
 <211> 408
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(385)
 <223> RXC2238

<400> 115
 ggcgatttagc caaaacatag agcggtaggc taagctatc agattgagca acatttcacg 60
 ctattaacac taatgtccat ataattttga aaagggtgca gtg acc aac gtg agc 115
 Val Thr Asn Val Ser
 1 5
 aac gag acc aac gcc acc aag gcc gtc ttc gat ccg cca gtg ggc att 163
 Asn Glu Thr Asn Ala Thr Lys Ala Val Phe Asp Pro Pro Val Gly Ile
 10 15 20
 acc gct cct ccg atc gat gaa ctg ctg gat aag gtc act tcc aag tac 211
 Thr Ala Pro Pro Ile Asp Glu Leu Leu Asp Lys Val Thr Ser Lys Tyr
 25 30 35
 gcc ctg gtg atc ttc gca gcc aag cgt gcg cgc cag atc aac agc ttc 259
 Ala Leu Val Ile Phe Ala Ala Lys Arg Ala Arg Gln Ile Asn Ser Phe
 40 45 50
 tac cat cag gca gat gag gga gta ttc gag ttc atc gga cca ttg gtt 307
 Tyr His Gln Ala Asp Glu Gly Val Phe Glu Phe Ile Gly Pro Leu Val
 55 60 65
 act ccg cag cca gcc gaa aag cca ctt tet att gct ctg cgt gag atc 355
 Thr Pro Gln Pro Gly Lys Lys Pro Leu Ser Ile Ala Leu Arg Glu Ile
 70 75 80 85
 aat gca ggt ctg ttg gac cac gag gaa ggt taaaagacct taaaacttca 405
 Asn Ala Gly Leu Leu Asp His Glu Glu Gly
 90 95

cac

408

12108 116

12111 35

12112 PRT

12113 Corynebacterium glutamicum

1400 116

Val Thr Asn Val Ser Asn Glu Thr Asn Ala Thr Lys Ala Val Phe Asp
1 5 10 15

Pro Pro Val Gly Ile Thr Ala Pro Pro Ile Asp Glu Leu Leu Asp Lys
20 25 30

Val Thr Ser Lys Tyr Ala Leu Val Ile Phe Ala Ala Lys Arg Ala Arg
35 40 45

Gln Ile Asn Ser Phe Tyr His Gln Ala Asp Glu Gly Val Phe Glu Phe
50 55 60

Ile Gly Pro Leu Val Thr Pro Gln Pro Gly Glu Lys Pro Leu Ser Ile
65 70 75 80

Ala Leu Arg Glu Ile Asn Ala Gly Leu Leu Asp His Glu Glu Gly
85 90 95

12110 117

12111 1927

12112 DNA

12113 Corynebacterium glutamicum

1400

12111 CDS

12112 (101)... (1804)

12113 RX000123

1400 117

ccattttccg ttgtgttttg cctaaagaac ccgatggaaa ttatcgtgaa gcaccgatcc 60

cggttatccg tctagagaca ccgtgggaag gggagcagca gtg agt aaa att tgg 115
Val Ser Lys Ile Ser
1 5

acg aaa ctc aag gcc ctg acc gcg gtg ctg tct gtg acc act ccg gtg 163
Thr Lys Leu Lys Ala Leu Thr Ala Val Leu Ser Val Thr Thr Leu Val
10 15 20

gct ggg tgt tcc aag ctt ccg cag aac acg gat ccg caa gtg ctg ccg 211
Ala Gly Cys Ser Thr Leu Pro Gln Asn Thr Asp Pro Gln Val Leu Arg
25 30 35

tca ttt tcc ggg tcc caa agc aca caa gag ata gca ggg ccg acc ccg 259
Ser Phe Ser Gly Ser Gln Ser Thr Gln Glu Ile Ala Gly Pro Thr Pro
40 45 50

aat caa gat ccg gat ttg ttg atc cgc ggc ttc ttc agc gca ggt gcg 307
Asn Gln Asp Pro Asp Leu Leu Ile Arg Gly Phe Phe Ser Ala Gly Ala
55 60 65

tat ccc aat cag cag tat gaa ggc ggc aag gcc tat ctg acg gaa ggg Tyr Pro Thr Gln Gln Tyr Glu Ala Ala Lys Ala Tyr Leu Thr Glu Gly 70 75 80 85	355
acg cgc agc acg tgg aat ccc gct ggc tgc act cgt att ttg gat cgt Thr Arg Ser Thr Trp Asn Pro Ala Ala Ser Thr Arg Ile Leu Asp Arg 90 95 100	403
att gat ctg aac act ctg cca ggt tgc acg aat gag gaa cga acg att Ile Asp Leu Asn Thr Leu Pro Gly Ser Thr Asn Ala Glu Arg Thr Ile 105 110 115	451
ggc atc cgt gga acg cag gtc gga acg ttg ctg agc ggt ggc gtg tat Ala Ile Arg Gly Thr Gln Val Gly Thr Leu Leu Ser Gly Gly Val Tyr 120 125 130	499
cag ccc gag aat ggc gag tta gaa gct gag atc gag atg cgt cca gaa Gln Pro Glu Asn Ala Glu Phe Glu Ala Glu Ile Thr Met Arg Arg Glu 135 140 145	547
gat ggg gat tgg cgt atc gat gct ttg ccc gat ggg att tta tta gag Asp Gly Glu Trp Arg Ile Asp Ala Leu Pro Asp Gly Ile Leu Leu Glu 150 155 160 165	595
aga aat gat ctg cgg aac cat taa act ccc car gat gtg tat tta tta Arg Asn Asp Leu Arg Asn His Tyr Thr Pro His Asp Val Tyr Phe Phe 170 175 180	643
gat ccc tta ggc cag gtg ttg gta ggc gat cgg cgt tgg ttg tta aat Asp Pro Ser Gly Gln Val Leu Val Gly Asp Arg Arg Trp Leu Phe Asn 185 190 195	691
gag tgc cag tgc atg tcc acg gtg ctg atg gcc ctt ctg gtt aat ggt Glu Ser Gln Ser Met Ser Thr Val Leu Met Ala Leu Leu Val Asn Gly 200 205 210	739
cct tgc ccc gca att tct cct ggt gtg gtc aat cag ctg tcc acg gat Pro Ser Pro Ala Ile Ser Pro Gly Val Val Asn Gln Leu Ser Thr Asp 215 220 225	787
ggc tgc ttc gtg ggg ttc aat gat ggg gag tat cag ttc act ggt ttg Ala Ser Phe Val Gly Phe Asn Asp Gly Glu Tyr Gln Phe Thr Gly Leu 230 235 240 245	835
gga aat ttg gat gat gat ggc cgt ttg cgt ttc gcc gcc cag gcc gtg Gly Asn Leu Asp Asp Asp Ala Arg Leu Arg Phe Ala Ala Gln Ala Val 250 255 260	883
tgg acg ttg ggc cat gct gat gtc gca gcc ccc tac act ttg gtc gct Trp Thr Leu Ala His Ala Asp Val Ala Gly Pro Tyr Thr Leu Val Ala 265 270 275	931
gac gcc ggc ccc ttg ctg tgc gag ttc cca acg ctg acc acc gat gac Asp Gly Ala Pro Leu Leu Ser Glu Phe Pro Thr Leu Thr Thr Asp Asp 280 285 290	979
ctc gcc gaa tac aac cca gag gct tac acc aac acg gtg tcc acg ttg Leu Ala Glu Tyr Asn Pro Glu Ala Tyr Thr Asn Thr Val Ser Thr Leu 295 300 305	1027

ttt gcg ttg cag gat gga tgg ttg tgg agg gtc agt tcc ggc aat gtg Phe Ala Leu Gln Asp Gly Ser Leu Ser Arg Val Ser Ser Gly Asn Val 310 315 320 325	1075
agt cca cta cag ggc att tgg agc ggt gga gat atc gat tct gca gcg Ser Pro Leu Gln Gly Ile Trp Ser Gly Gly Asp Ile Asp Ser Ala Ala 330 335 340	1123
att tcc tcc tcc ggc aat gtg gtg gca gcg gta cgc cac gaa aac aac Ile Ser Ser Ser Ala Asn Val Val Ala Ala Val Arg His Glu Asn Asn 345 350 355	1171
gag gca gtg ctt act gtt ggc tcc atg gaa ggc gtg act tca gat ggt Glu Ala Val Leu Thr Val Gly Ser Met Glu Gly Val Thr Ser Asp Ala 360 365 370	1219
ttg agg agt gaa acg atc act cgt ccc acc ttt gaa tac gcg tgg agt Leu Arg Ser Glu Thr Ile Thr Arg Pro Thr Phe Glu Tyr Ala Ser Ser 375 380 385	1267
ggg ttg ttg ggt ttg gtg gat ttg gag agt cct gtc cga ttc gca gta Gly Leu Trp Ala Val Val Asp Gly Glu Thr Pro Val Arg Val Ala Arg 390 395 400 405	1315
tcc gca aca acc ggt gag ctc gtc cag acg gag gcg gag att gtg ctt Ser Ala Thr Thr Gly Glu Leu Val Gln Thr Glu Ala Glu Ile Val Leu 410 415 420	1363
cca agg gat gtg acg ggt ccc atc tct gaa ttc caa ctg tca cga act Pro Arg Asp Val Thr Gly Pro Ile Ser Glu Phe Gln Leu Ser Arg Thr 425 430 435	1411
ggg gtc ggg ggc gaa atg atc att gaa ggc aag gtg tac gtg ggc gta Gly Val Arg Ala Ala Met Ile Ile Glu Gly Lys Val Tyr Val Gly Val 440 445 450	1459
gta acg cgt cct ggt ccc ggc gag cgg cgc gtg aca aat atc acg gag Val Thr Arg Pro Gly Pro Gly Glu Arg Arg Val Thr Asn Ile Thr Glu 455 460 465	1507
gtg gcg ccc agc ttg ggc gag gcg gcg ctg tgg atc aac tgg cgc cca Val Ala Pro Ser Leu Gly Glu Ala Ala Leu Ser Ile Asn Trp Arg Pro 470 475 480 485	1555
gac ggc att ttg ctt gtg ggc acg tca att cca gag acg ccc ctg tgg Asp Gly Ile Leu Leu Val Gly Thr Ser Ile Pro Glu Thr Pro Leu Trp 490 495 500	1603
cgc gtc gag cag gac gga tgg gcg att tgg tgg atg ccc agc ggg aat Arg Val Glu Gln Asp Gly Ser Ala Ile Ser Ser Met Pro Ser Gly Asn 505 510 515	1651
ctc agc gcg ccc gtg gtg gcg gtg gca agt tcc gcg acg acg gtc tac Leu Ser Ala Pro Val Val Ala Val Ala Ser Ser Ala Thr Thr Val Tyr 520 525 530	1699
gtc act gat tgg cat ggc atg ctt cag ctg ccc act gcc gat aat gat Val Thr Asp Ser His Ala Met Leu Gln Leu Pro Thr Ala Asp Asn Asp 535 540 545	1747
att tgg cgc gag gtg ccc ggt ttg ctg gcc acg cgt ggt ggc ccc gtg	1795

Ile Trp Arg Glu Val Pro Gly Leu Leu Gly Thr Arg Ala Ala Pro Val
 550 555 560 565

gtt gcg tac tgatggagct gttcttcccg cgc
 Val Ala Tyr

1827

<210> 118

<211> 568

<212> FRT

<213> Corynebacterium glutamicum

<400> 118

Val Ser Lys Ile Ser Thr Lys Leu Lys Ala Leu Thr Ala Val Leu Ser
 1 5 10 15

Val Thr Thr Leu Val Ala Gly Cys Ser Thr Leu Pro Gln Asn Thr Asp
 20 25 30

Pro Gln Val Leu Arg Ser Phe Ser Gly Ser Gln Ser Thr Gln Glu Ile
 35 40 45

Ala Gly Pro Thr Pro Asn Gln Asp Pro Asp Leu Leu Ile Arg Gly Phe
 50 55 60

Phe Ser Ala Gly Ala Tyr Pro Thr Gln Gln Tyr Gln Ala Ala Lys Ala
 65 70 75 80

Tyr Leu Thr Glu Gly Thr Arg Ser Thr Trp Asn Pro Ala Ala Ser Tar
 85 90 95

Arg Ile Leu Asp Arg Ile Asp Leu Asn Thr Leu Pro Gly Ser Thr Asn
 100 105 110

Ala Glu Arg Thr Ile Ala Ile Arg Gly Thr Gln Val Gly Thr Leu Leu
 115 120 125

Ser Gly Gly Val Tyr Gln Pro Glu Asn Ala Glu Phe Glu Ala Glu Ile
 130 135 140

Thr Met Arg Arg Glu Asp Gly Glu Trp Arg Ile Asp Ala Leu Pro Asp
 145 150 155 160

Gly Ile Leu Leu Glu Arg Asn Asp Leu Arg Asn His Tyr Thr Pro His
 165 170 175

Asp Val Tyr Phe Phe Asp Pro Ser Gly Gln Val Leu Val Gly Asp Arg
 180 185 190

Arg Trp Leu Phe Asn Glu Ser Gln Ser Met Ser Thr Val Leu Met Ala
 195 200 205

Leu Leu Val Asn Gly Pro Ser Pro Ala Ile Ser Pro Gly Val Val Asn
 210 215 220

Gln Leu Ser Thr Asp Ala Ser Phe Val Gly Phe Asn Asp Gly Glu Tyr
 225 230 235 240

Gln Phe Thr Gly Leu Gly Asn Leu Asp Asp Asp Ala Arg Leu Arg Phe
 245 250 255

Ala Ala Gln Ala Val Trp Thr Leu Ala His Ala Asp Val Ala Gly Pro
 260 265 270
 Tyr Thr Leu Val Ala Asp Gly Ala Pro Leu Leu Ser Glu Phe Pro Thr
 275 280 285
 Leu Thr Thr Asp Asp Leu Ala Glu Tyr Asn Pro Glu Ala Tyr Thr Asn
 290 295 300
 Thr Val Ser Thr Leu Phe Ala Leu Gln Asp Gly Ser Leu Ser Arg Val
 305 310 315 320
 Ser Ser Gly Asn Val Ser Pro Leu Gln Gly Ile Trp Ser Gly Gly Asp
 325 330 335
 Ile Asp Ser Ala Ala Ile Ser Ser Ser Ala Asn Val Val Ala Ala Val
 340 345 350
 Arg His Glu Asn Asn Glu Ala Val Leu Thr Val Gly Ser Met Glu Gly
 355 360 365
 Val Thr Ser Asp Ala Leu Arg Ser Glu Thr Ile Thr Arg Pro Thr Phe
 370 375 380
 Glu Tyr Ala Ser Ser Gly Leu Trp Ala Val Val Asp Gly Glu Thr Pro
 385 390 395 400
 Val Arg Val Ala Arg Ser Ala Thr Thr Gly Glu Leu Val Gln Thr Glu
 405 410 415
 Ala Glu Ile Val Leu Pro Arg Asp Val Thr Gly Pro Ile Ser Glu Phe
 420 425 430
 Gln Leu Ser Arg Thr Gly Val Arg Ala Ala Met Ile Ile Glu Gly Lys
 435 440 445
 Val Tyr Val Gly Val Val Thr Arg Pro Gly Pro Gly Glu Arg Arg Val
 450 455 460
 Thr Asn Ile Thr Glu Val Ala Pro Ser Leu Gly Glu Ala Ala Leu Ser
 465 470 475 480
 Ile Asn Trp Arg Pro Asp Gly Ile Leu Leu Val Gly Thr Ser Ile Pro
 485 490 495
 Glu Thr Pro Leu Trp Arg Val Glu Gln Asp Gly Ser Ala Ile Ser Ser
 500 505 510
 Met Pro Ser Gly Asn Leu Ser Ala Pro Val Val Ala Val Ala Ser Ser
 515 520 525
 Ala Thr Thr Val Tyr Val Thr Asp Ser His Ala Met Leu Gln Leu Pro
 530 535 540
 Thr Ala Asp Asn Asp Ile Trp Arg Glu Val Pro Gly Leu Leu Gly Thr
 545 550 555 560
 Arg Ala Ala Pro Val Val Ala Tyr
 565

<210> 119
 <211> 1344
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1321)
 <223> RXA02240

<400> 119
 cagctagagac acgacacattg cagctttaga cagcttggtc tatattgggtt tattgtattt 60
 aagaattattt attctaaact tcttcgaaag aagggtattt ggg gat cag cca acc 115
 Val Ala Gln Pro Thr
 1 5
 gcc gtc cgt ttg ttc acc agt gaa tct gta act gag gga cat cca gac 163
 Ala Val Arg Leu Phe Thr Ser Glu Ser Val Thr Gln Gly His Pro Asp
 10 15 20
 aaa ata tat gat gct att taa gac aat att tag gag ggg ctg atc aaa 211
 Lys Ile Cys Asp Ala Ile Ser Asp Thr Ile Leu Asp Ala Leu Leu Glu
 25 30 35
 aaa gat cag cag tcc cgc gtc gaa ggg gaa act ggg gtc acc acc gga 259
 Lys Asp Pro Gln Ser Arg Val Ala Val Glu Thr Val Val Thr Thr Gly
 40 45 50
 atc gtc cat gtt gtt ggc cag gtc cgt acc ggc ggt tac gta gag atc 307
 Ile Val His Val Val Gly Glu Val Arg Thr Ser Ala Tyr Val Glu Ile
 55 60 65
 cct caa tta gtc cgc aac aag ctc atc gaa atc gga ttc aac tcc tct 355
 Pro Gln Leu Val Arg Asn Lys Leu Ile Glu Ile Gly Phe Asn Ser Ser
 70 75 80 85
 gag gtt gga ttc gac gga cgc acc tgt ggc gtc tca gta tcc atc ggt 403
 Glu Val Gly Phe Asp Gly Arg Thr Cys Gly Val Ser Val Ser Ile Gly
 90 95 100
 gag cag tcc cag gaa atc gct gac ggc gtg gat aac tcc gac gaa gcc 451
 Glu Gln Ser Gln Glu Ile Ala Asp Gly Val Asp Asn Ser Asp Glu Ala
 105 110 115
 cgc acc aac ggc gac gtt gaa gaa gac gac cgc gca ggt gct ggc gac 499
 Arg Thr Asn Gly Asp Val Glu Glu Asp Asp Arg Ala Gly Ala Gly Asp
 120 125 130
 cag ggc ctg atg ttc ggc tac gcc acc aac gaa acc gaa gag tac atg 547
 Gln Gly Leu Met Phe Gly Tyr Ala Thr Asn Glu Thr Glu Glu Tyr Met
 135 140 145
 cct ctt cct atc ggc ttg ggc cac cga ctg tca cgt cgt ctg acc cag 595
 Pro Leu Pro Ile Ala Leu Ala His Arg Leu Ser Arg Arg Leu Thr Gln
 150 155 160 165
 gtt cgt aaa gag ggc atc gtt cct cac ctg cgt cca gac gga aaa acc 643
 Val Arg Lys Glu Gly Ile Val Pro His Leu Arg Pro Asp Gly Lys Thr
 170 175 180

cag gtc acc ttc gca tac gat gag caa gac cgc cct agc cac ctg gat	691
Gln Val Thr Phe Ala Tyr Asp Ala Gln Asp Arg Pro Ser His Leu Asp	
185 190 195	
acc gtt gtc atc tcc acc cag cac gac cca gaa gtt gac cgt gca tgg	739
Thr Val Val Ile Ser Thr Gln His Asp Pro Glu Val Asp Arg Ala Trp	
200 205 210	
ttg gaa acc caa ctg cgc gaa cac gtc att gat tgg gta atc aaa gac	787
Leu Glu Thr Gln Leu Arg Glu His Val Ile Asp Trp Val Ile Lys Asp	
215 220 225	
gca ggc att gag gat ctg gca acc ggt gag atc acc gtg ttg atc aac	835
Ala Gly Ile Glu Asp Leu Ala Thr Gly Glu Ile Thr Val Leu Ile Asn	
230 235 240 245	
cct tca gtt ttt ttt att ctg ggt ggt cca atg ggt gat gct ggt ctg	883
Pro Ser Gly Ser Phe Ile Leu Gly Gly Pro Met Gly Asp Ala Gly Leu	
250 255 260	
acc ggc cca aag atc atc gtg gat acc tac ggt ggc atg gct cgc cat	931
Thr Gly Arg Lys Ile Ile Val Asp Thr Tyr Gly Gly Met Ala Arg His	
265 270 275	
ggt gtt tta gta ttt tcc ggt gag gat tca agc aag gta gat ggt ttt	979
Gly Gly Gly Ala Phe Ser Gly Lys Asp Pro Ser Lys Val Asp Arg Ser	
280 285 290	
gct gca tac gct atg cgt tgg gta gca aag aac atc gtg gca gca ggc	1027
Ala Ala Tyr Ala Met Arg Trp Val Ala Lys Asn Ile Val Ala Ala Gly	
295 300 305	
ctt gct gat cgc gct gaa gtt cag gtt gca tac gcc att gga cgc gca	1075
Leu Ala Asp Arg Ala Glu Val Gln Val Ala Tyr Ala Ile Gly Arg Ala	
310 315 320 325	
aag cca gtc gga ctt tac gtt gaa acc ttt gac acc aac aag gaa ggc	1123
Lys Pro Val Gly Leu Tyr Val Glu Thr Phe Asp Thr Asn Lys Glu Gly	
330 335 340	
ctg agc gac gag cag att cag gct gcc gtg ttg gag gtc ttt gac ctg	1171
Leu Ser Asp Glu Gln Ile Gln Ala Ala Val Leu Glu Val Phe Asp Leu	
345 350 355	
cgt cca gca gca att atc cgt gag ctt gat ctg ctt cgt ccg atc tac	1219
Arg Pro Ala Ala Ile Ile Arg Glu Leu Asp Leu Leu Arg Pro Ile Tyr	
360 365 370	
gct gac act gct gcc tac ggc cac ttt ggt cgc act gat ttg gac ctt	1267
Ala Asp Thr Ala Ala Tyr Gly His Phe Gly Arg Thr Asp Leu Asp Leu	
375 380 385	
cct tgg gag gct atc gac cgc gtt gat gaa ctt cgc gca gcc ctg aag	1315
Pro Trp Glu Ala Ile Asp Arg Val Asp Glu Leu Arg Ala Ala Leu Lys	
390 395 400 405	
ttg gcc taataatctg atgtagtatc ttc	1344
Leu Ala	

<210> 120
 <211> 407
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 120

Val	Ala	Gln	Pro	Thr	Ala	Val	Arg	Leu	Phe	Thr	Ser	Glu	Ser	Val	Thr
1				5					10					15	
Glu	Gly	His	Pro	Asp	Lys	Ile	Cys	Asp	Ala	Ile	Ser	Asp	Thr	Ile	Leu
			20					25					30		
Asp	Ala	Leu	Leu	Gln	Lys	Asp	Pro	Gln	Ser	Arg	Val	Ala	Val	Glu	Thr
		35					40					45			
Val	Val	Thr	Thr	Gly	Ile	Val	His	Val	Val	Gly	Glu	Val	Arg	Thr	Ser
	50				55						60				
Ala	Tyr	Val	Glu	Ile	Pro	Gln	Leu	Val	Arg	Asn	Lys	Leu	Ile	Glu	Ile
65					70					75				80	
Gly	Phe	Asn	Ser	Ser	Glu	Val	Gly	Phe	Asp	Gly	Arg	Thr	Cys	Gly	Val
			85						90					95	
Ser	Val	Ser	Ile	Gly	Glu	Gln	Ser	Gln	Glu	Ile	Ala	Asp	Gly	Val	Asp
			100					105					110		
Asn	Ser	Asp	Glu	Ala	Arg	Thr	Asn	Gly	Asp	Val	Glu	Glu	Asp	Asp	Arg
		115					120					125			
Ala	Gly	Ala	Gly	Asp	Gln	Gly	Leu	Met	Phe	Gly	Tyr	Ala	Thr	Asn	Glu
	130					135					140				
Thr	Glu	Glu	Tyr	Met	Pro	Leu	Pro	Ile	Ala	Leu	Ala	His	Arg	Leu	Ser
145					150					155					160
Arg	Arg	Leu	Thr	Gln	Val	Arg	Lys	Glu	Gly	Ile	Val	Pro	His	Leu	Arg
			165						170					175	
Pro	Asp	Gly	Lys	Thr	Gln	Val	Thr	Phe	Ala	Tyr	Asp	Ala	Gln	Asp	Arg
		180						185					190		
Pro	Ser	His	Leu	Asp	Thr	Val	Val	Ile	Ser	Thr	Gln	His	Asp	Pro	Glu
		195					200					205			
Val	Asp	Arg	Ala	Trp	Leu	Glu	Thr	Gln	Leu	Arg	Glu	His	Val	Ile	Asp
	210					215					220				
Trp	Val	Ile	Lys	Asp	Ala	Gly	Ile	Glu	Asp	Leu	Ala	Thr	Gly	Glu	Ile
225					230					235				240	
Thr	Val	Leu	Ile	Asn	Pro	Ser	Gly	Ser	Phe	Ile	Leu	Gly	Gly	Pro	Met
			245						250					255	
Gly	Asp	Ala	Gly	Leu	Thr	Gly	Arg	Lys	Ile	Ile	Val	Asp	Thr	Tyr	Gly
		260					265						270		
Gly	Met	Ala	Arg	His	Gly	Gly	Gly	Ala	Phe	Ser	Gly	Lys	Asp	Pro	Ser
	275					280						285			

Lys Val Asp Arg Ser Ala Ala Tyr Ala Met Arg Trp Val Ala Lys Asn
 290 295 300

Ile Val Ala Ala Gly Leu Ala Asp Arg Ala Glu Val Gln Val Ala Tyr
 305 310 315 320

Ala Ile Gly Arg Ala Lys Pro Val Gly Leu Tyr Val Glu Thr Phe Asp
 325 330 335

Thr Asn Lys Glu Gly Leu Ser Asp Glu Gln Ile Gln Ala Ala Val Leu
 340 345 350

Glu Val Phe Asp Leu Arg Pro Ala Ala Ile Ile Arg Glu Leu Asp Leu
 355 360 365

Leu Arg Pro Ile Tyr Ala Asp Thr Ala Ala Tyr Gly His Phe Gly Arg
 370 375 380

Thr Asp Leu Asp Leu Pro Trp Glu Ala Ile Asp Arg Val Asp Glu Leu
 385 390 395 400

Arg Ala Ala Leu Lys Leu Ala
 405

<E10> 121

<E11> 23

<E12> DNA

<E13> Artificial Sequence

<E20>

<E23> Description of Artificial Sequence: primer

<F00> 121

taggatatac ggcgtacactt aga

23

<E10> 122

<E11> 23

<E12> DNA

<E13> Artificial Sequence

<E20>

<E23> Description of Artificial Sequence: primer

<F00> 122

BBAAACCGGG GCATCGAAAC TTA

23

<E10> 123

<E11> 18

<E12> DNA

<E13> Artificial Sequence

<E20>

<E23> Description of Artificial Sequence: primer

<F00> 123

ggaaacagta tgaccatg

18

<210> 124
 <211> 17
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: primer

<400> 124
 gtaaaaacgac agccagc

18

<210> 125
 <211> 4334
 <212> DNA
 <213> Corynebacterium glutamicum

<400> 125
 aaatggtttt aaatgagag gtcgggttat gattttttt tgaagagactg gctcgttgaa 60
 gaaatctat aaagatatgt ctgaatttag ttttttttt tgaacgttga atagagtaatt 120
 taagtctggt ggaattgaac ttccacgagg atgtgttga tttccacagt aaatgttgaa 180
 tctcgttggt gtaaaaagggt tccccacgtt ggggttttt tcttgggcctt cttttctaggt 240
 cggcctgatt gattctgaag ctctctaggg ggggttttt tatagggcaga taaagggttc 300
 ccacccgggtt acctcgttaag cgcacaagga ctgcttctaa agatcttcaa agccactgct 360
 ggcactccgt ttgcggaagc cttgccccgt gaaattttt tccacgaggt tegtgcacac 420
 cctatctgaa agctctcttc acctaaaatt agagagattt gattcttacc gtggaaaatt 480
 ttgcacaaaa tcttcccttg atcgcccttg cgaattttt cgggggggtg cggctgggtg 540
 cgtttgggtt gacagaattg atcagcttgc atgctgttag gtgcagggat ccccggggtg 600
 gaaagccacg tctgtcttca aaatctctga tgttacattg caaagataa aaatatatca 660
 tcatgaacaa taaaactgtc tctttacata aacagtaata caaggggtgt tatgagccat 720
 attcaacggg aaacgtcttg ctcgagggcg cgattaaatt ccaacatgga tctctgattt 780
 tatgggtata aatgggctcg cgataatgtc gggcaatcag gtgcgacaat ctatcgattg 840
 tatgggaagc ccgatgcgcc agagttgttt ctgaaacatg gcaaaggtag cgttgccaat 900
 gatgttacag atgagatggt cagactaaac tggctgaagg aatttatgcc tcttcgcacc 960
 atcaageatt ttatcgttac tctgatgat gcatggttac tcaccactgc gatccccggg 1020
 aaaacagcat tccaggtatt agaagaatat cctgatttag gtgaaaatat tgttgatgcg 1080
 ctggcagtgt tctgcgcgc gttgcattcg attcctgttt gtaattgttc ttttaacaga 1140
 gatcgggtat ttctctctgc tcaggcgcaa ttaagaatga ataacggttt ggttgatgcg 1200
 agtgattttg atgaagagcg taatggctgg cctgttgaa atgtctggaa agaaatgcac 1260
 aagctttttg cttctctacc ggattcagtc gtaactcttg gtgatttttc acttgataac 1320

cttattttttg acgaggggaa attaataggt tgtattgatg ttggacgagt oggaatcgca 1340
gaccgatacc aggatctttg catcctatgg aactgcctcg gtgagtttcc tccctcatta 1440
cagaaacggg tttttcaaaa atatggtatt gataatcctg atatgaataa attgcagttt 1500
catttgatgc cogatgaggt tttctaatca gaactgggta attggttgta acactggcag 1560
agcattacgc tgaacttgac ggacgggggg tttgttgaat aaatcgaaact tttgctgagt 1600
tgaaggatca gatcaagcat cttcccgaca acccagacccg ctccgtggca aagcaaaaagt 1640
tcaaaatcac caactgggta acctacaaca aagctctcat caacccgtggc tccctcactt 1700
tcctggctgga ccatgggggg attcaggcct ggtatgagtc agcaacaccc tcttcacgag 1760
gcagacctca gggcccccga attgatcagt actggggcgt cgtcgatcgc cctcgagagc 1800
ctgtgggggt ggcttgctcc tgaggggcgt gcgacagata gctaaaaato tgcgtcagga 1860
tcggcgtaga gggcggtcgt cgtcgactgg aggttctccc ttgggttgac ggtcttcaat 1900
cgtctacggc ccatcccgac gctctctctg tgcgtacgtt ccatcgtttt attctcgtcg 2000
atcccgaaaa agttctctgc tcttgtaaaa aactctctcg tcggcccgca aattctcgat 2040
tcagatcttc ttaaaaaaca agccagaaat accacacacg gtttcagat aatccgtctt 2100
tcggaaaaat caagtgcgat acaaaaattt tagcacccct gagctgcgca aagtcccgct 2160
tcgtgaaaaa cctcgtgcgt cgtgattctt cgcacaaaaa tttaacgaac gttcgttata 2200
atgggtgatc gaccttcacg accaagtacc aaaattgggc cgaatcatca gctatggatc 2240
tcctcgatgt cggcctggag tcggacgggc ccatcgctgc cgtcgattta aaaaagggtg 2300
tcggatcttc ccgagctctc gatccgacgg accggccagc accacgagac tgggcacgtg 2360
ccggcagcga cctagaaaat ctcgtggcgg atcttgagga gctggctgac gagctggcgt 2400
ctcggcagcg ccaggaggac gcacagtagt ggaggatcga accagttcgt cctactggcg 2460
tggcctgatt cctcccccgt ctgacccggc aggaacgggc gcaaaaatatt gctcagatgc 2500
gtgtcgtgac gcagccagcc gcgagcggcg caacaaaacyc caccgcgagg agctggaggc 2560
ggctaggtcg caaatggcgc tggaaagtgc tcccccgagc gaaatttttg ccatggtcgt 2600
cacagagctg gaagcggcag ccagaattat ccgcgatcgt ggcggcgtgc ccgcagccat 2660
gacaaacatc gtaaatgcgc cgtttcgtgt ggcctgtggc gccacggacg tgcacggcgc 2700
gccaccact gccaccgaac gccagcagcg tcgcgcgtcg aaaaagcgca caggcggcaa 2760
gaagcgataa gctgcacgaa tacctgaaaa atgttgaaac ccccgtagac ggtaactcac 2800
agggcgtcgg ctaacccccg gtcacaaaca gggagaaagc gtcacaaaat gactctagcg 2860
gattcacgag acattgacac accgycctgg aaattttcgc ctgatctgtt cgacacccat 2920

cccgagctcg cgttgcgac acgtggctgg acgagcgaag aacgcgcgca atttctcgct 3180
cacctgggca gagaataatt ccagggcagc aagaccccg agttcgccag cgtttggatc 3240
aaagaccocg acacgggaga aacacagccg aagttatacc gatttggttc aaaatcgctt 3300
gcccggctgc agtatgttgc tctgaagcag gcgcagcag ccagcgtgct tctcctggac 3360
attgatgtgc cagaccacca gcccgccggg aaaatcgagc acgtaaaccc cagagctctac 3420
gggattttgg agcgttggc acgcctggaa aaagcgccag ctgggatcgg cgtgaatcca 3480
ctgagcgggg aatgcacagc catctggctc attgatccgg tctatgcgc agcagggcatg 3540
agcagcccca atctgcgcct gctggctgca acgacccagg aaatgacccg cgttttcggc 3600
gagcaccagg ctttttcaa taggtcgagc cgggtggcag tgcagctctc agcagatcac 3660
aacgcgtacc cgtggcatgc ccagcacaat cgcctggatc gctagctga tcttatggag 3720
attctcgca cttctcagg acagaaaaa cctaaaaaa gctatgagca cttttttt 3780
agcggacggg caggtatcga agcggcaga aaagcactg ccgagcaca aaactttgc 3840
acgtttgaag caactctc tagcgcctc gaagcctc gacagctgat cagcggcctc 3900
cgtctcctct gactgcctc agggcctc gccctc atg agcagcttc cagcagctc 3960
ctgactgtgg gataccagtt aaaagcgcct ggtgagcgc taaaagacac cagatcctc 4020
gacgcctacg aggtgcctc caccgtcctc caggcgtcgc gacagacgg cgtgagcct 4080
gatctgcgc cgtatgcgtg ccgcacagac atggcgcgac gctgctgcgg ctactcgct 4140
aaagccacg cagtcctcct cctcctcag acagacagc agagcagcc agggcgaaaa 4200
gctctggcca atctgggaag acgtggcgtt aaaaaggcc cagacgctg gaaagaccca 4260
aacagtgagt aagcccgagc acagcgagaa aaactagct agtcagctc acgacaagct 4320
aggaaagcta aagg 4334